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<b>(21) International Application Number:</b> PCT/US98/09998 <b>(22) International Filing Date:</b> 15 May 1998 (15.05.98)  <b>(30) Priority Data:</b> 08/857,886 16 May 1997 (16.05.97) US 60/062,893 20 October 1997 (20.10.97) US 60/069,719 16 December 1997 (16.12.97) US 1465/97 16 December 1997 (16.12.97) DK  <b>(71) Applicants:</b> NOVO NORDISK BIOTECH, INC. [US/US]; 1445 Drew Avenue, Davis, CA 95616-4880 (US). NOVO NORDISK A/S [DK/DK]; Novo Alle, DK-2880 Bagsvaerd (DK). ASAHI CHEMICAL INDUSTRY CO., LTD. [JP/JP]; 2-1, Samejima, Fuji-City, Shizuoka, Tokyo 416 (JP).			<b>(72) Inventors:</b> BLINKOVSKY, Alexander; 955 Cranbrook Court #306, Davis, CA 95616 (US). BROWN, Kimberly; 8322 Windswept Court, Elk Grove, CA 95758 (US). GO- LIGHTLY, Elizabeth; Apartment 171, 1880 Cowell Boule- vard, Davis, CA 95616 (US). BYUN, Tony; Apart- ment A, 841 Adams Terrace, Davis, CA 95616 (US). MATHIANSEN, Thomas, E.; Nordborggade 3, DK-2100 Copenhagen Ø (DK). KOFOD, Lene, V.; Brorfeldevej 8, DK-4350 Uggeløse (DK). FUJII, Mikio; 466-5, Miyashita, Fuji-shi, Shizuoka 416 (JP). MARUMOTA, Chigusa; 576-1, Kona, Izunagaoka-cho, Shizuoka 410-22 (JP).  <b>(74) Agents:</b> ZELSON, Steve, T. et al.; Novo Nordisk of North America, Inc., Suite 6400, 405 Lexington Avenue, New York, NY 10174 (US).  <b>(81) Designated States:</b> AL, AU, BB, BG, BR, CA, CN, CU, CZ, EE, GE, HU, IL, IS, JP, KP, KR, LC, LK, LR, LT, LU, LV, MG, MK, MN, MX, NO, NZ, PL, RO, SG, SI, SK, TR, TT, UA, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i> <i>With an indication in relation to deposited biological material furnished under Rule 13bis separately from the description.</i>
<b>(54) Title:</b> METHODS OF PRODUCING PROTEIN HYDROLYSATES			
<b>(57) Abstract</b>  The present invention relates to methods of producing protein hydrolysates, comprising adding to a proteinaceous material one or more aminopeptidase(s) having glycine releasing properties and one or more additional proteases wherein the amount of glycine produced is greater than the amount of glycine produced by the one or more additional proteases alone under the same conditions.			

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## METHODS OF PRODUCING PROTEIN HYDROLYSATES

### Cross-Reference to Related Applications

This application is a continuation-in-part of pending U.S. application no. 08/857,886 filed May 16, 1997, and claims priority of Danish application no. 1465/97 filed December 16, 1997, and U.S. provisional application nos. 60/062,893 and 60/069,719 filed October 20, 1997 and December 16, 1997, respectively, which applications are fully incorporated herein by reference.

### Background of the Invention

#### Field of the Invention

The present invention relates to methods of producing a protein hydrolysate, comprising adding to a proteinaceous material one or more polypeptide(s) having glycine releasing activity and one or more additional proteases wherein the amount of glycine produced is greater than the amount of glycine produced by the one or more additional proteases alone under the same conditions.

#### Description of the Related Art

Various food products, *e.g.*, soups, sauces and seasonings, contain flavoring agents obtained by hydrolysis of proteinaceous materials. This hydrolysis is conventionally accomplished using strong hydrochloric acid, followed by neutralization with sodium hydroxide. However, such chemical hydrolysis leads to severe degradation of the amino acids obtained during the hydrolysis, and also to hazardous byproducts formed in the course of this chemical reaction. Increasing concern over the use of flavoring agents obtained by chemical hydrolysis has led to the development of enzymatic hydrolysis processes.

Enzymatic hydrolysis processes of proteinaceous materials aim at obtaining a high degree of hydrolysis (DH), and this is usually attained using a complex of unspecific acting proteolytic enzymes (*i.e.*, unspecific-acting endo- and exo-peptidases). For example, WO 94/25580 describes a method for hydrolyzing proteins by use of an unspecific acting

enzyme preparation obtained from *Aspergillus oryzae*. Specific acting proteolytic enzymes have not been used for this purpose because such enzymes only lead to an inadequate degree of hydrolysis.

Polypeptides having aminopeptidase activity catalyze the removal of one or more amino acid residues from the N-terminus of peptides, polypeptides, and proteins. Such polypeptides are classified under the Enzyme Classification Number E.C. 3.4.11.- of the International Union of Biochemistry and Molecular Biology.

WO 96/28542 discloses an aminopeptidase which has a molecular weight of 35 kDa. JP-7-5034631 (Noda) discloses a leucine aminopeptidase obtained from yellow koji mold, which includes *Aspergillus oryzae*. JP-7-4021798 (Zaidan Hojin Noda Sangyo) discloses the production of miso by adding a leucine aminopeptidase II prepared by cultivating a number of strains, including *Aspergillus oryzae* strain 460 (ATCC 20386) and strain IAM 2616. *Aspergillus oryzae* strain 460 is known to produce a number of leucine aminopeptidases of which three have a molecular weight of 26.5, 56, and 61 kDa by gel filtration (Nakada *et al.*, 1972, *Agricultural and Biological Chemistry* 37: 757-765; Nakada *et al.*, 1972, *Agricultural and Biological Chemistry* 37: 767-774; and Nakada *et al.*, 1972, *Agricultural and Biological Chemistry* 37: 775-782; respectively). *Penicillium citrium* produces an intracellular leucine aminopeptidase with a molecular weight of 65 kDa by SDS-PAGE (Kwon *et al.*, 1996, *Journal of Industrial Microbiology* 17: 30-35).

WO 97/04108 (Roehm) discloses DNA encoding an *Aspergillus sojae* leucine aminopeptidase. Chang and Smith (1989, *Journal of Biological Chemistry* 264: 6979-6983) disclose the molecular cloning and sequencing of a gene encoding a vacuolar aminopeptidase from *Saccharomyces cerevisiae*. Chang *et al.* (1992, *Journal of Biological Chemistry* 267: 8007-8011) disclose the molecular cloning and sequencing of a gene encoding a methionine aminopeptidase from *Saccharomycse cerevisiae*.

The production of protein hydrolysates with desirable organoleptic properties and high degrees of hydrolysis generally requires the use of a mixture of peptidase activities. It would be desirable to provide a single component peptidase enzyme which has activity useful for improving the organoleptic properties and degree of hydrolysis of protein hydrolysates used in food products either alone or in combination with other enzymes.

It is an object of the present invention to provide improved methods for producing protein hydrolysates with desirable organoleptic qualities and/or high degrees of hydrolysis.

## Summary of the Invention

The present invention relates to method of producing a protein hydrolysate, comprising adding to a proteinaceous material one or more aminopeptidase(s) having glycine releasing properties and one or more additional proteases wherein the amount of glycine produced is greater than the amount of glycine produced by the one or more additional proteases alone under the same conditions.

## Brief Description of the Figures

Figure 1 shows the nucleic acid sequence and the deduced amino acid sequence of an *Aspergillus oryzae* ATCC 20386 aminopeptidase (SEQ ID NOS:1 and 2, respectively).

Figure 2 shows a restriction map of pMWR3.

Figure 3 shows a restriction map of pEJG19.

Figure 4 shows a restriction map of pDM181.

Figure 5 shows a restriction map of pEJG28.

Figure 6 shows the activity of a *Sphingomonas capsulata* aminopeptidase versus pH measured at room temperature using a 100 mg/ml solution of Ala-pNA in DMSO.

Figure 7 shows the activity of a *Sphingomonas capsulata* aminopeptidase versus the temperature in 50 mM sodium phosphate buffer pH 7.5.

Figure 8 shows the activity of a *Sphingomonas capsulata* aminopeptidase versus the temperature in 50 mM sodium phosphate buffer pH 7.5.

Figure 9 shows the effect on the DH when adding a *Sphingomonas capsulata* crude enzyme extract and a *Sphingomonas capsulata* aminopeptidase to respectively low and high Flavourzyme™ background dosage.

Figure 10 shows the effect on the DH when adding a *Sphingomonas capsulata* crude enzyme extract and a *Sphingomonas capsulata* aminopeptidase to respectively low and high Flavourzyme™ background dosage.

Figure 11 shows the DH obtained by different combinations of Flavourzyme™, Alcalase® and a *Sphingomonas capsulata* aminopeptidase.

Figure 12 showins the DH obtained by different combinations of Flavourzyme™, Alcalase® and a *Sphingomonas capsulata* aminopeptidase.

### Detailed Description of the Invention

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The present invention relates to method of producing a protein hydrolysate, comprising adding to a proteinaceous material one or more polypeptide(s) having glycine releasing activity and one or more additional proteases wherein the amount of glycine produced is greater than the amount of glycine produced by the one or more additional proteases alone under the same conditions. Because of the activity of the glycine-releasing polypeptide, the methods of the present invention are able to produce protein hydrolysates having a higher degree of hydrolysis or the same degree of hydrolysis using lower amounts of enzyme.

In a preferred embodiment, the amount of glycine produced is between 10-400%, preferably 50-350%, more preferably 100-350%, even more preferably 150-350%, and most preferably 200-350%, than the amount of glycine produced by the one or more additional proteases under the same conditions..

The enzymatic treatment(s) may take place at any convenient temperature at which the enzymes do not become inactivated, preferably in the range of from about 20°C to about 70°C. In accordance with established practice, the enzymes may be inactivated by increasing the temperature of the incubation mixture to a temperature where the enzymes become inactivated, *e.g.*, to above about 70°C, or by decreasing the pH of the incubation mixture to a point where the enzymes become inactivated, *e.g.*, below about 4.0.

In a preferred embodiment, the methods of the present invention produce a protein hydrolysate having a degree of hydrolysis between 35-90%, preferably 45-80%, more preferably 50-75%, even more preferably 55-75%, and most preferably 60-70%.

The degree of hydrolysis (DH) is the percentage of the total number of amino bonds in a protein that has been hydrolyzed by a proteolytic enzyme. The DH is defined by the following formula:

$$\text{DH} = \frac{\text{Number of peptide bonds cleaved}}{\text{Total number of peptide bonds}} \times 100\%$$

The DH may be calculated according to Adler-Nissen; Enzymic Hydrolysis of Food Proteins; Elsevier Applied Science Publishers Ltd. (1986), page 122.

## 5 Proteinaceous Material

The methods of the present invention comprise treating a proteinaceous material with at least two enzymes. The proteinaceous material may consist of intact proteins, prehydrolyzed proteins (*i.e.*, peptides), or a mixture thereof.

10 In a preferred embodiment, the proteinaceous material is a foodstuff. The proteinaceous material may be of vegetable or animal origin.

In another preferred embodiment, the proteinaceous material is of animal origin, preferably milk protein, whey protein, casein, meat protein, fish protein, blood protein, egg white gelatin, or lactalbumin.

15 In another preferred embodiment, the proteinaceous material is of vegetable origin, preferably soy protein, grain proteins, *e.g.*, wheat gluten, corn gluten, barley, rye, oat, rice, zein, lupine, cotton seed protein, rape seed protein, peanut, alfalfa protein, pea protein, fabaceous bean protein, sesame seed protein, or sunflower.

## Polypeptides Having Glycine Releasing Activity

20 One of the enzymes added to the proteinaceous material is a polypeptide having glycine releasing activity. The term "glycine releasing activity" is defined herein as a peptidase activity which catalyzes the removal of glycine from the N-terminal end of peptides, oligopeptides or proteins. The polypeptides may also have peptidase activity which is capable of cleaving one or more amino acids X from the N-terminus of a peptide, 25 polypeptide, or protein, wherein X represents any amino acid residue selected from the group consisting of Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, and Val, but at least Leu, Glu, Gly, Ala, and/or Pro.

The polypeptide(s) may be added to the proteinaceous substrate in an effective amount conventionally employed in protein hydrolysis processes, preferably in the range of 30 from about 0.1 to about 100,000 aminopeptidase units per 100 g of protein, and more preferably in the range of from about 1 to about 10,000 aminopeptidase units per 100 g of protein. As defined herein, one aminopeptidase unit (APU) is the amount of enzyme

needed to release 1 micromole of p-nitroanilide per minute from Leu-p-nitroanilide (Sigma Chemical Co., St. Louis MO) under the specified conditions. Alternatively, the aminopeptidase may be employed preferably in the range of from about 0.5 to about 500 LAPU/g of protein, and more preferably in the range of from about 5 to about 50 LAPU/g of protein. LAPU is defined as the leucine aminopeptidase activity which is determined as described in AF 298/1-GB (available on request from Novo Nordisk A/S, Denmark).

In a preferred embodiment, the polypeptide preferentially cleaves glycine.

In another preferred embodiment, the polypeptide is selected from the group consisting of:

(a) a polypeptide having an amino acid sequence which has at least 50% identity with the amino acid sequence of SEQ ID NO:2;

(b) a polypeptide encoded by a nucleic acid sequence which hybridizes under medium stringency conditions with (i) the nucleic acid sequence of SEQ ID NO:1, (ii) its complementary strand, or (iii) a subsequence thereof;

(c) an allelic variant of (a) or (b); and

(d) a fragment of (a), (b), or (c), wherein the fragment has aminopeptidase activity;

and

(e) a polypeptide having aminopeptidase activity with physicochemical properties of (i) a pH optimum in the range of from about pH 7.27 to about pH 10.95 determined at ambient temperature in the presence of Ala-para-nitroanilide; (ii) a temperature stability of 90% or more, relative to initial activity, at pH 7.5 determined after incubation for 20 minutes at 60°C in the absence of substrate; and (iii) an activity towards Xaa-para-nitroanilide wherein Xaa is selected from the group consisting of Leu, Glu, Gly, Ala, and Pro.

In another preferred embodiment, the polypeptide is selected from the group consisting of:

(a) a polypeptide having an amino acid sequence which has at least 50% identity with the amino acid sequence of SEQ ID NO:11;

(b) a polypeptide encoded by a nucleic acid sequence which hybridizes under medium stringency conditions with (i) the nucleic acid sequence of SEQ ID NO:10, (ii) its complementary strand, or (iii) a subsequence thereof;

(c) an allelic variant of (a) or (b); and

(d) a fragment of (a), (b), or (c), wherein the fragment has aminopeptidase activity; and

(e) a polypeptide which (a) has aminopeptidase activity in the pH range between pH 5.0-8.5 measured at 37°C, (b) an isoelectric point (pI) in the range of 7.4-8.5; (c) has aminopeptidase activity in the temperature range of 20-55°C, measured at pH 7.5 using Gly-pNA in Tris-HCl buffer; (d) hydrolyzes Ala-pNA, Gly-pNA, Leu-pNA, Glu-pNA, Asp-pNA, Lys-pNA, Ile-pNA and Val-pNA; (e) does not hydrolyze Phe-pNA nor Pro-pNA; (f) is not inhibited by phenylmethanesulfonyl fluoride, slightly inhibited by EDTA, di-isopropyl fluoro phosphate, p-chloromercuribenzoic acid and iodoacetic acid, completely inhibited by o-phenanthroline, and/or (g) is obtained from a strain belonging to *Sphingomonas* and has a molecular mass of  $67 \pm 5$  kDa.

In a preferred embodiment, the polypeptide has an amino acid sequence which has a degree of identity to the amino acid sequence of SEQ ID NO:2 or 11 of at least about 50%, preferably at least about 60%, preferably at least about 70%, more preferably at least about 80%, even more preferably at least about 90%, most preferably at least about 95%, and even most preferably at least about 97%, which have aminopeptidase activity (hereinafter "homologous polypeptides"). In a preferred embodiment, the homologous polypeptides have an amino acid sequence which differs by five amino acids, preferably by four amino acids, more preferably by three amino acids, even more preferably by two amino acids, and most preferably by one amino acid from the amino acid sequence of SEQ ID NO:2 or 11. For purposes of the present invention, the degree of identity between two amino acid sequences is determined by the Clustal method (Higgins, 1989, *CABIOS* 5: 151-153) with an identity table, a gap penalty of 10, and a gap length penalty of 10.

Preferably, the polypeptides comprise the amino acid sequence of SEQ ID NO:2 or 11, an allelic variant; and a fragment thereof, wherein the fragment has aminopeptidase activity. In a more preferred embodiment, the polypeptides comprise the amino acid sequence of SEQ ID NO:2 or 11. In another preferred embodiment, the polypeptide has the amino acid sequence of SEQ ID NO:2 or 11 or a fragment thereof, wherein the fragment has aminopeptidase activity. A fragment of SEQ ID NO:2 is a polypeptide having one or more amino acids deleted from the amino and/or carboxy terminus of this amino

acid sequence. In a most preferred embodiment, the polypeptide has the amino acid sequence of SEQ ID NO:2 or 11.

Preferably, a fragment contains at least 330 amino acid residues, more preferably at least 380 amino acid residues, and most preferably at least 430 amino acid residues.

5 An allelic variant denotes any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in phenotypic polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequences. The term allelic variant is also used to denote a protein encoded by an allelic  
10 variant of a gene.

The amino acid sequences of the homologous polypeptides may differ from the amino acid sequence of SEQ ID NO:2 or 11 by an insertion or deletion of one or more amino acid residues and/or the substitution of one or more amino acid residues by different amino acid residues. Preferably, amino acid changes are of a minor nature, that is  
15 conservative amino acid substitutions that do not significantly affect the folding and/or activity of the protein; small deletions, typically of one to about 30 amino acids; small amino- or carboxyl-terminal extensions, such as an amino-terminal methionine residue; a small linker peptide of up to about 20-25 residues; or a small extension that facilitates purification by changing net charge or another function, such as a poly-histidine tract, an  
20 antigenic epitope or a binding domain.

Examples of conservative substitutions are within the group of basic amino acids (such as arginine, lysine and histidine), acidic amino acids (such as glutamic acid and aspartic acid), polar amino acids (such as glutamine and asparagine), hydrophobic amino acids (such as leucine, isoleucine and valine), aromatic amino acids (such as phenylalanine,  
25 tryptophan and tyrosine), and small amino acids (such as glycine, alanine, serine, threonine and methionine). Amino acid substitutions which do not generally alter the specific activity are known in the art and are described, for example, by H. Neurath and R.L. Hill, 1979, *In, The Proteins*, Academic Press, New York. The most commonly occurring exchanges are Ala/Ser, Val/Ile, Asp/Glu, Thr/Ser, Ala/Gly, Ala/Thr, Ser/Asn, Ala/Val, Ser/Gly,  
30 Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu, and Asp/Gly as well as these in reverse.

In another preferred embodiment, the polypeptide are encoded by nucleic acid sequences which hybridize under low stringency conditions, more preferably medium stringency conditions, and most preferably high stringency conditions, with an oligonucleotide probe which hybridizes under the same conditions with the nucleic acid sequence of SEQ ID NO:1 or 10 or their complementary strand (J. Sambrook, E.F. Fritsch, and T. Maniatus, 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York); or allelic variants and fragments of the polypeptides, wherein the fragments have aminopeptidase activity.

Hybridization indicates that the nucleic acid sequence hybridizes to the oligonucleotide probe corresponding to the polypeptide encoding part of the nucleic acid sequence shown in SEQ ID NO:1 or 10, under low to high stringency conditions (*i.e.*, prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 µg/ml sheared and denatured salmon sperm DNA, and either 25, 35 or 50% formamide for low, medium and high stringencies, respectively), following standard Southern blotting procedures.

The amino acid sequence of SEQ ID NO:2 or 11 or a partial sequence thereof may be used to design an oligonucleotide probe, or a nucleic acid sequence encoding a polypeptide of the present invention, such as the nucleic acid sequence of SEQ ID NO:1 or 10, or a subsequence thereof, may be used to identify and clone DNA encoding polypeptides having aminopeptidase activity from strains of different genera or species according to methods well known in the art. In particular, such probes can be used for hybridization with the genomic or cDNA of the genus or species of interest, following standard Southern blotting procedures, in order to identify and isolate the corresponding gene therein. Such probes can be considerably shorter than the entire sequence, but should be at least 15, preferably at least 25, and more preferably at least 40 nucleotides in length. Longer probes can also be used. Both DNA and RNA probes can be used. The probes are typically labeled for detecting the corresponding gene (for example, with <sup>32</sup>P, <sup>3</sup>H, <sup>35</sup>S, biotin, or avidin).

Thus, a genomic, cDNA or combinatorial chemical library prepared from such other organisms may be screened for DNA which hybridizes with the probes described above and which encodes a polypeptide having aminopeptidase activity. Genomic or other DNA from such other organisms may be separated by agarose or polyacrylamide gel electrophoresis, or other separation techniques. DNA from the libraries or the separated DNA may be

transferred to and immobilized on nitrocellulose or other suitable carrier material. In order to identify a clone or DNA which is homologous with SEQ ID NO:1 or 10, the carrier material is used in a Southern blot in which the carrier material is finally washed three times for 30 minutes each using 2 x SSC, 0.2% SDS preferably at least 50°C, more preferably at least 55°C, more preferably at least 60°C, more preferably at least 65°C, even more preferably at least 70°C, and most preferably at least 75°C. Molecules to which the oligonucleotide probe hybridizes under these conditions are detected using X-ray film.

In another preferred embodiment, the polypeptides have the following physicochemical properties: (a) a pH optimum in the range of from about pH 7.27 to about pH 10.95 determined at ambient temperature in the presence of Ala-para-nitroanilide; (ii) a temperature stability of 90% or more, relative to initial activity, at pH 7.5 determined after incubation for 20 minutes at 60°C in the absence of substrate; and (iii) an activity towards Xaa-para-nitroanilide wherein Xaa is selected from the group consisting of Leu, Glu, Gly, Ala, and Pro. The polypeptides also have the ability to hydrolyze other substrates.

In a preferred embodiment, the pH optimum in the range of from about pH 7.27 to about pH 10.95, more preferably in the range of from about pH 8.03 to about pH 10.95, and most preferably in the range of from about pH 8.62 to about pH 10.51 determined after incubation for 5 minutes at ambient temperature in the presence of Ala-Pro-para-nitroanilide.

In another preferred embodiment, the polypeptide has a molecular mass of  $67 \pm 5$  kDa, more preferably a molecular mass of  $67 \pm 2$  kDa and is obtained from a strain belonging to *Sphingomonas*, more preferably *Sphingomonas capsulata* and most preferably *Sphingomonas capsulata* IFO 12533. The molecular mass is measured by SDS-polyacrylamide gel electrophoresis (SDS-PAGE) using a 10-15% gradient gel on the apparatus of FAST System from Pharmacia (Uppsala, Sweden). The molecular mass of the enzyme was estimated from the regression line of molecular weight markers as follows:

phosphorylase b (94 kDa)

albumin (67 kDa)

ovalbumin (43 kDa)

carbonic anhydrase (30 kDa)

trypsin inhibitor (20.1 kDa)

a-lactalbumine (14.4 kDa)

In another preferred embodiment, the polypeptide (a) has aminopeptidase activity in the pH range between pH 5.0-8.5 measured at 37°C, more preferably in the pH range 6.5-8.0, and even more preferably having the highest aminopeptidase activity in the pH range 7.0-7.5 measured at 37°C; (b) an isoelectric point (pI) in the range of 7.4-8.5; (c) has aminopeptidase activity in the temperature range of 20-55°C, measured at pH 7.5 using Gly-pNA in Tris-HCl buffer; (d) hydrolyzes Ala-pNA, Gly-pNA, Leu-pNA, Glu-pNA, Asp-pNA, Lys-pNA, Ile-pNA and Val-pNA; (e) does not hydrolyze Phe-pNA nor Pro-pNA; and/or (f) is not inhibited by phenylmethanesulfonyl fluoride, slightly inhibited by EDTA, di-isopropyl fluoro phosphate, p-chloromercuribenzoic acid and iodoacetic acid, completely inhibited by o-phenanthroline.

The isoelectric point of the aminopeptidase is variable since the pI of the freshly prepared enzyme is estimated as 8.4 using an activity staining method, however, pI varies to 7.4 - 8.5 during the course of purification and/or storage. The uncertainty of pI may be due to the self digestion of the aminopeptidase from its amino terminal.

In a more preferred embodiment, the polypeptide is obtained from an *Aspergillus oryzae* strain, and most preferably from *Aspergillus oryzae* ATCC 20386 or a mutant strain thereof, e.g., the polypeptide with the amino acid sequence of SEQ ID NO:2.

In another preferred embodiment, the polypeptide is obtained from a *Sphingomonas capsulata* strain, e.g., *Sphingomonas capsulata* is IFO 12533, which is a bacterial strain kept at the Institute for Fermentation, Osaka, Japan, e.g., the polypeptide with the amino acid sequence of SEQ ID NO:11 (the predicted signal peptide consists of the first 32 amino acids).

In another embodiment, the polypeptides have immunochemical identity or partial immunochemical identity to the polypeptide having the amino acid sequence of SEQ ID NO:2 or 11. The immunochemical properties are determined by immunological cross-reaction identity tests by the well-known Ouchterlony double immunodiffusion procedure. Specifically, an antiserum containing antibodies which are immunoreactive or bind to epitopes of the polypeptide having the amino acid sequence of SEQ ID NO:2 or 11 are prepared by immunizing rabbits (or other rodents) according to the procedure described by Harboe and Ingild, In N.H. Axelsen, J. Krøll, and B. Weeks, editors, *A Manual of*

*Quantitative Immunelectrophoresis*, Blackwell Scientific Publications, 1973, Chapter 23, or Johnstone and Thorpe, *Immunochemistry in Practice*, Blackwell Scientific Publications, 1982 (more specifically pages 27-31). A polypeptide having immunochemical identity is a polypeptide which reacts with the antiserum in an identical fashion such as total fusion of precipitates, identical precipitate morphology, and/or identical electrophoretic mobility using a specific immunochemical technique. A further explanation of immunochemical identity is described by Axelsen, Bock, and Krøll, *In* N.H. Axelsen, J. Krøll, and B. Weeks, editors, *A Manual of Quantitative Immunelectrophoresis*, Blackwell Scientific Publications, 1973, Chapter 10. A polypeptide having partial immunochemical identity is a polypeptide which reacts with the antiserum in a partially identical fashion such as partial fusion of precipitates, partially identical precipitate morphology, and/or partially identical electrophoretic mobility using a specific immunochemical technique. A further explanation of partial immunochemical identity is described by Bock and Axelsen, *In* N.H. Axelsen, J. Krøll, and B. Weeks, editors, *A Manual of Quantitative Immunelectrophoresis*, Blackwell Scientific Publications, 1973, Chapter 11.

Polypeptides encoded by nucleic acid sequences which hybridize with an oligonucleotide probe which hybridizes with the nucleic acid sequence of SEQ ID NO:1 or 10, their complementary strands, or allelic variants and subsequences of SEQ ID NO:1 or 10; allelic variants and fragments of the polypeptides; or the homologous polypeptides and polypeptides having identical or partially identical immunological properties may be obtained from microorganisms of any genus.

In a preferred embodiment, these polypeptides may be obtained from a bacterial source. For example, these polypeptides may be obtained from a gram positive bacterium such as a *Bacillus* strain, *e.g.*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus stearothermophilus*, *Bacillus subtilis*, or *Bacillus thuringiensis*; or a *Streptomyces* strain, *e.g.*, *Streptomyces lividans* or *Streptomyces murinus*; or from a gram negative bacterium, *e.g.*, *E. coli* or *Pseudomonas* sp.

The polypeptides may be obtained from a fungal source, and more preferably from a yeast strain such as a *Candida*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomyces*, or *Yarrowia* strain; or a filamentous fungal strain such as an *Acremonium*, *Aspergillus*, *Aureobasidium*, *Cryptococcus*, *Filibasidium*, *Fusarium*,

*Humicola*, *Magnaporthe*, *Mucor*, *Myceliophthora*, *Neocallimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Piromyces*, *Schizophyllum*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Tolypocladium*, or *Trichoderma* strain.

In a preferred embodiment, the polypeptides are obtained from a *Saccharomyces*  
5 *carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis* or *Saccharomyces oviformis* strain.

In another preferred embodiment, the polypeptides are obtained from a *Fusarium*  
10 *bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecioides*, *Fusarium venenatum*, *Humicola insolens*, *Humicola lanuginosa*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*, *Penicillium*  
15 *purpurogenum*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei*, or *Trichoderma viride* strain.

The polypeptides are preferably obtained from species of *Aspergillus* including, but not limited to, *Aspergillus aculeatus*, *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger*, or *Aspergillus oryzae*.

20 It will be understood that for the aforementioned species, the invention encompasses both the perfect and imperfect states, and other taxonomic equivalents, e.g., anamorphs, regardless of the species name by which they are known. Those skilled in the art will readily recognize the identity of appropriate equivalents. The polypeptides may also be obtained from microorganisms which are synonyms of *Aspergillus* as defined by Raper,  
25 K.D. and Fennel, D.I., 1965, *The Genus Aspergillus*, The Wilkins Company, Baltimore. *Aspergilli* are mitosporic fungi characterized by an aspergillum comprised of a conidiospore stipe with no known teleomorphic states terminating in a vesicle, which in turn bears one or two layers of synchronously formed specialized cells, variously referred to as sterigmata or phialides, and asexually formed spores referred to as conidia. Known teleomorphs of  
30 *Aspergillus* include *Eurotium*, *Neosartorya*, and *Emericella*. Strains of *Aspergillus* and teleomorphs thereof are readily accessible to the public in a number of culture collections, such as the American Type Culture Collection (ATCC), Deutsche Sammlung von

Mikroorganismen und Zellkulturen GmbH (DSM), Centraalbureau Voor Schimmelcultures (CBS), and Agricultural Research Service Patent Culture Collection, Northern Regional Research Center (NRRL).

Furthermore, such polypeptides may be identified and obtained from other sources including microorganisms isolated from nature (*e.g.*, soil, composts, water, etc.) using the above-mentioned probes. Techniques for isolating microorganisms from natural habitats are well known in the art. The nucleic acid sequence may then be derived by similarly screening a genomic or cDNA library of another microorganism. Once a nucleic acid sequence encoding the polypeptide has been detected with the probe(s), the sequence may be isolated or cloned by utilizing techniques which are known to those of ordinary skill in the art (see, *e.g.*, Sambrook *et al.*, 1989, *supra*).

For purposes of the present invention, the term "obtained from" as used herein in connection with a given source shall mean that the polypeptide is produced by the source or by a cell in which a gene from the source has been inserted.

The polypeptide(s) may be a fused polypeptides or cleavable fusion polypeptides in which another polypeptide is fused at the N-terminus or the C-terminus of the polypeptide or fragment thereof. A fused polypeptide is produced by fusing a nucleic acid sequence (or a portion thereof) encoding another polypeptide to a nucleic acid sequence (or a portion thereof) of the present invention. Techniques for producing fusion polypeptides are known in the art, and include ligating the coding sequences encoding the polypeptides so that they are in frame and that expression of the fused polypeptide is under control of the same promoter(s) and terminator.

#### **Additional Protease(s)**

In the methods of the present invention, the proteinaceous material also is treated with one or more additional proteases. The additional protease(s) may be added simultaneously with the polypeptide(s) or consecutively. The additional protease(s) may be added to the proteinaceous material in an effective amount conventionally employed in protein hydrolysis processes.

The one or more additional proteases may be endopeptidases. The endopeptidase(s) may be added to the proteinaceous substrate in an effective amount conventionally employed in protein hydrolysis processes, preferably in the range of from about 0.05 to

about 15 AU/100 g of protein, and more preferably from about 0.1 to about 8 AU/100 g of protein. One AU (Anson Unit) is defined as the amount of enzyme which under standard conditions (*i.e.*, 25°C, pH 7.5 and 10 min. reaction time) digests hemoglobin at an initial rate such that there is liberated per minute an amount of TCA soluble product which gives  
5 the same color with phenol reagent as one milli-equivalent of tyrosine. The analytical method AF 4/5 is available upon request from Novo Nordisk A/S, Denmark, which is incorporated herein by reference.

In a preferred embodiment, the endopeptidase is a glutamyl endopeptidase (EC 3.4.21.19); a lysyl endopeptidase (EC 3.4.21.50); a leucyl endopeptidase (EC 3.4.21.57); a  
10 glycyl endopeptidase (EC 3.4.22.25); a prolyl endopeptidase (EC 3.4.21.26); trypsin (EC 3.4.21.4) or a trypsin-like (lysine/arginine specific) endopeptidase; or a peptidyl-Asp metalloendopeptidase (EC 3.4.24.33).

The glutamyl endopeptidase (EC 3.4.21.19) may preferably be obtained from a *Bacillus* strain, in particular *Bacillus licheniformis* and *Bacillus subtilis*, a *Staphylococcus*  
15 strain, in particular *Staphylococcus aureus*, a *Streptomyces* strain, in particular *Streptomyces thermovulgaris* and *Streptomyces griseus*, or a *Actinomyces* strain.

The lysyl endopeptidase (EC 3.4.21.50) may preferably be obtained from a *Achromobacter* strain, in particular *Achromobacter lyticus*, a *Lysobacter* strain, in particular *Lysobacter enzymogenes*, or a *Pseudomonas* strain, in particular *Pseudomonas*  
20 *aeruginosa*.

The leucyl endopeptidase (EC 3.4.21.57) may be of plant origin.

The glycyl endopeptidase (EC 3.4.22.25) may preferably be obtained from the papaya plant (*Carica papaya*).

The prolyl endopeptidase (EC 3.4.21.26) may preferably be obtained from a  
25 *Flavobacterium* strain, or it may be of plant origin.

The trypsin-like endopeptidase may preferably be obtained from a *Fusarium* strain, in particular *Fusarium oxysporum*, *e.g.*, as described in WO 89/06270 or WO 94/25583.

The peptidyl-Asp metalloendopeptidase (EC 3.4.24.33) may preferably be obtained from a *Pseudomonas* strain, in particular *Pseudomonas fragi*.

30 The endopeptidase may be obtained from a strain of *Bacillus*, preferably *Bacillus amyloliquefaciens*, *Bacillus lentus*, *Bacillus licheniformis* or *Bacillus subtilis*, a strain of *Staphylococcus*, preferably *Staphylococcus aureus*, a strain of *Streptomyces*, preferably

*Streptomyces thermovularis* or *Streptomyces griseus*, a strain of *Actinomyces* species, a strain of *Aspergillus*, preferably *Aspergillus aculeatus*, *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus nidulans*, *Aspergillus niger*, *Aspergillus oryzae*, or *Aspergillus sojae*, or a strain of *Fusarium*, preferably *Fusarium venenatum*.

5 In another preferred embodiment, the specific acting proteolytic enzyme is an exopeptidase that may act from either end of the peptide.

In a preferred embodiment, the exopeptidase is an aminopeptidase such as a leucyl aminopeptidase (EC 3.4.11.1); a dipeptide aminopeptidase or a tripeptide aminopeptidase (EC 3.4.11.4).

10 In another preferred embodiment, the exopeptidase is a carboxypeptidase such as a proline carboxypeptidase (EC 3.4.16.2); a carboxypeptidase A (EC 3.4.17.1); a carboxypeptidase B (EC 3.4.17.2); a carboxypeptidase C (EC 3.4.16.5); a carboxypeptidase D (EC 3.4.16.6); a lysine (arginine) carboxypeptidase (EC 3.4.17.3); a glycine carboxypeptidase (EC 3.4.17.4); an alanine carboxypeptidase (EC 3.4.17.6); a  
15 glutamate carboxypeptidase (EC 3.4.17.11); a peptidyl-dipeptidase A (EC 3.4.15.1); or a peptidyl-dipeptidase (EC 3.4.15.5).

In a most preferred embodiment, the additional protease is a plurality of proteases sold under the name FLAVOURZYME™ manufactured by Novo Nordisk A/S, Denmark. The protease formulation contains at least five *Aspergillus oryzae*-derived proteases and  
20 peptidases of different molecular weight.

### Additional Enzymes

In a preferred embodiment, the proteinaceous material is treated with one or more additional enzymes. The one or more additional enzymes may be an amylase,  
25 carbohydrase, cellulase, esterase, alpha-galactosidase, beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase, lipase, pectinolytic enzyme, peptidoglutaminase, phytase, transglutaminase, or xylanase.

The additional enzyme(s) may be obtained from a microorganism belonging to the genus *Aspergillus*, preferably *Aspergillus aculeatus*, *Aspergillus awamori*, *Aspergillus  
30 niger*, or *Aspergillus oryzae*, *Trichoderma*, *Humicola*, preferably *Humicola insolens*, or *Fusarium*, preferably *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium*

*heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecioides*, or *Fusarium venenatum*.

5

### Protein Hydrolysates

The present invention also relates to protein hydrolysates produced by the methods of the present invention.

The present invention also relates to protein hydrolysates enriched in free glutamic acid and/or peptide bound glutamic acid residues. Such protein hydrolysates can be produced by subjecting the proteinaceous material to a deamidation process either prior to or simultaneously with the enzymatic treatment(s).

These protein hydrolysates have excellent flavor because glutamic acid (Glu), whether free or peptide bound, plays an important role in the flavor and palatability of protein hydrolysates. These protein hydrolysates also have improved functionality, in particular, improved solubility, improved emulsifying properties, increased degree of hydrolysis, and improved foaming properties.

The deamidation process, *i.e.*, the conversion of amides (glutamine or asparagine) into charged acids (glutamic acid or aspartic acid) via the liberation of ammonia, may take place as a non-enzymatic or as an enzymatic deamidation process.

In a preferred embodiment, the deamidation is carried out as an enzymatic deamidation process, *e.g.*, by subjecting the substrate to a transglutaminase and/or peptidoglutaminase.

The transglutaminase may be of any convenient source including mammals, see *e.g.*, JP 1050382 and JP 5023182, including activated Factor XIII, see *e.g.*, WO 93/15234; those derived from fish, see *e.g.*, EP 555,649; and those obtained from microorganisms, see *e.g.*, EP 379,606, WO 96/06931 and WO 96/22366. In a preferred embodiment, the transglutaminase is obtained from an Oomycete, including a strain of *Phytophthora*, preferably *Phytophthora cactorum*, or a strain of *Pythium*, preferably *Pythium irregulare*, *Pythium* sp., *Pythium intermedium*, *Pythium ultimum*, or *Pythium periplocum* (or *Pythium periplocum*). In another preferred embodiment, the transglutaminase is of bacterial origin and is obtained from a strain of *Bacillus*, preferably *Bacillus subtilis*, a strain of

*Streptoverticillium*, preferably *Streptoverticillium mobaraensis*, *Streptoverticillium griseocarneum*, or *Streptoverticillium cinnamoneum*, and a strain of *Streptomyces*, preferably *Streptomyces lydicus*.

The peptidoglutaminase may be a peptidoglutaminase I (peptidyl-glutaminase; EC 3.5.1.43), or a peptidoglutaminase II (protein-glutamine glutaminase; EC 3.5.1.44), or any mixture thereof. The peptidoglutaminase may be obtained from a strain of *Aspergillus*, preferably *Aspergillus japonicus*, a strain of *Bacillus*, preferably *Bacillus circulans*, a strain of *Cryptococcus*, preferably *Cryptococcus albidus*, or a strain of *Debaryomyces*, preferably *Debaryomyces hansenii*.

The transglutaminase is added to the proteinaceous substrate in an effective amount conventionally employed in deamidation processes, preferably in the range of from about 0.01 to about 5% (w/w), and more preferably in the range of from about 0.1 to about 1% (w/w) of enzyme preparation relating to the amount of substrate.

The peptidoglutaminase is added to the proteinaceous substrate in an effective amount conventionally employed in deamidation processes, preferably in the range of from about 0.01 to about 100,000 PGase Units per 100 g of substrate, and more preferably in the range of from about 0.1 to about 10,000 PGase Units per 100 g of substrate.

The peptidoglutaminase activity may be determined according to the procedure of Cedrangoro *et al.* (1965, *Enzymologia* 29: 143). According to this procedure, 0.5 ml of an enzyme sample, adjusted to pH 6.5 with 1 N NaOH, is charged into a small vessel. Then 1 ml of a borate pH 10.8 buffer solution is added to the vessel. The discharged ammonia is absorbed by 5 N sulphuric acid, and by use of Nessler's reagent the mixture is allowed to form color which is measured at 420 nm. One PGase unit is the amount of enzyme capable of producing 1 micromole of ammonia per minute under these conditions.

Alternatively, the peptidoglutaminase activity may be determined according to the procedure described in US 3,857,967 or Example 20 below.

The present invention also relates to food products, *e.g.*, baked products, and animal feed additives comprising a protein hydrolysate obtained by the methods of the present invention. Such food products exhibit enhanced organoleptic qualities, such as improvement in flavor, palatability, mouth feel, aroma and crust color.

In the present context, the term "baked products" includes any food prepared from dough, either of a soft or a crisp character. Examples of baked products, whether of a

white, light or dark type, which may be advantageously produced by the present invention, are bread, in particular white, whole-meal or rye bread, typically in the form of loaves or rolls; French baguette-type breads; pita breads; tacos; cakes; pancakes; biscuits; crisp breads; and the like.

5        Such baked products are conventionally prepared from a dough which comprises flour and water, and which is typically leavened. The dough may be leavened in various ways, such as by adding sodium bicarbonate or the like, or by adding a leaven (fermenting dough), but the dough is preferably leavened by adding a suitable yeast culture such as a culture of *Saccharomyces cerevisiae* (baker's yeast). Any of the commercially available  
10 *Saccharomyces cerevisiae* strains may be employed.

Further, the dough used in the preparation of the baked products may be fresh or frozen. The preparation of frozen dough is described by K. Kulp and K. Lorenz in "Frozen and Refrigerated Doughs and Batters". A flavor improving composition of the present invention is typically included in the dough in an amount in the range of 0.01-5%,  
15 more preferably 0.1-3%.

The present invention also relates to the use of a hydrolysate produced by the methods of the invention as an additive to food products, such as baked foods, to enhance organoleptic qualities, such as flavor, palatability and aroma.

The present invention is further described by the following examples which should  
20 not be construed as limiting the scope of the invention.

### Examples

#### Example 1: Purification of FLAVOURZYME™ aminopeptidase II

25        Aminopeptidase was purified from a FLAVOURZYME™ broth (Novo Nordisk A/S, Bagsværd, Denmark). The FLAVOURZYME™ broth was produced by cultivation of *Aspergillus oryzae* strain 1568 (ATCC 20386) in a medium composed of carbon and nitrogen sources and trace metals. First, the broth (20 ml containing 720 mg of protein) was diluted with 180 ml of 20 mM sodium phosphate pH 7.0 buffer and filtered using  
30 Nalgene Filterware equipped with a 0.45 µm filter (Nalgene, Rochester, NY). The filtered solution was loaded onto a 24 x 130 mm column containing 31 ml of Q-Sepharose, Big Beads (Pharmacia Biotech AB, Uppsala, Sweden) pre-equilibrated with 20 mM sodium

phosphate pH 7.0 buffer. The protein was eluted using pH gradients from 7.0 (20 mM sodium phosphate buffer) to 5.0 (20 mM sodium acetate buffer), from 5.0 to 3.5 (20 mM sodium acetate buffer), and then from 3.5 to 3.0 (20 mM sodium acetate buffer). Fractions eluting between pH 3.5 and 3.0 were collected, pooled, and concentrated to 20 ml by  
5 ultrafiltration with a PM 10 membrane (Amicon, New Bedford, MA).

The concentrated solution was diluted with 100 ml of 20 mM sodium phosphate pH 7.0 buffer and then loaded onto a 20 x 100 mm column containing Pharmacia MonoQ Beads (Pharmacia Biotech AB, Uppsala, Sweden) pre-equilibrated with 20 mM sodium phosphate pH 7.0 buffer. The protein was eluted with a 0 to 0.4 M NaCl gradient in 20  
10 mM sodium phosphate pH 7.0 buffer. The fractions between 0.330 and 0.343 M NaCl were collected, pooled, and concentrated using ultrafiltration against 20 mM sodium acetate pH 4.0 buffer.

The purified preparation was found to contain three major bands judged by SDS-PAGE analysis. The sample consisted of components with molecular weights of  
15 approximately 65, 50 and 33 kDa.

#### **Example 2: Amino acid sequencing of aminopeptidase II**

An aliquot of the purified aminopeptidase II preparation described in Example 1 was electrophoresed and subsequently blot-transferred to a PVDF membrane (Novex, San  
20 Diego, CA) using 10 mM CAPS (3-[cyclohexylamino]-1-propanesulfonic acid) pH 11 in 10% methanol for 2 hours. The PVDF membrane was stained with 0.1% Coomassie Blue R-250 in 40% methanol/1% acetic acid for 20 seconds and destained in 50% ethanol to observe the protein bands. Three components at 65, 50, and 33 kDa were excised and subjected to amino terminal sequencing on an Applied Biosystems Model 476A Protein  
25 Sequencer (Applied Biosystems, Inc., Foster City, CA) using a blot cartridge and liquid phase TFA delivery according to the manufacturer's instructions. All three components yielded the same amino terminal sequence, RALVSPDEFPEDIQLEDLLEGSQQLEDFAY (SEQ ID NO:2).

A 300 µl sample of the protein was dried on a Savant Speed Vac AS160 (Savant  
30 Instruments, Farmingdale, NY) and then reconstituted with 300 µl of 70% formic acid (aqueous). A few crystals of cyanogen bromide were added and incubated at room temperature in the dark overnight. The sample was redried in the Speed Vac and

reconstituted in Tricine sample buffer (Novex, San Diego, CA). The cyanogen bromide cleavage fragments were separated using a 10-20% Tricine SDS-polyacrylamide gel into bands of 6, 10, 15, 22, 27, 40 and 50 kDa and blot-transferred to a PVDF membrane. The 6, 10, 15, and 22 kDa bands were excised and subjected to amino terminal sequencing.

5        The amino terminal sequences of the 15 and 22 kDa bands were identical to the amino terminal sequence above, while the sequences of the 6 and 10 kDa bands were both determined to contain the sequence TYSPSVEVTADVAVVKNLGTSEADYPDVEGKVAL (SEQ ID NO:2).

### 10    **Example 3: *Aspergillus oryzae* strain 1568 RNA isolation**

*Aspergillus oryzae* strain 1568 was cultivated in a fermentation tank in a medium composed of 7.5 g of potato starch, 10 g of soy bean meal, 2 g of  $\text{KH}_2\text{PO}_4$ , 5 g of  $\text{Na}_2\text{HPO}_4 \cdot 2\text{H}_2\text{O}$ , and 0.1 g of  $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$  per liter. A two liter sample was taken after five days of growth at 30°C, and the mycelia were collected, frozen in liquid  $\text{N}_2$ , and  
15    stored at -80°C. Total RNA was prepared from the frozen, powdered mycelia of *Aspergillus oryzae* 1568 by extraction with guanidinium thiocyanate followed by ultracentrifugation through a 5.7 M cesium chloride cushion (Chirgwin *et al.*, 1979, *Biochemistry* 18: 5294-5299). Poly(A)+ RNA was isolated by oligo(dT)-cellulose affinity chromatography according to Aviv and Leder (1972, *Proceedings of the National Academy of Sciences USA* 69: 1408-1412).  
20   

### **Example 4: Construction of a cDNA library**

      Double-stranded cDNA was synthesized from 5 µg of *Aspergillus oryzae* 1568 poly(A)+ RNA of Example 3 using the procedure described by Gubler and Hoffman  
25    (1983, *Gene* 25: 263-269) and Sambrook *et al.* (1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, New York), except that an oligo(dT)-*NotI* anchor primer, instead of an oligo(dT)12-18 primer, was used in the first strand reaction. After synthesis, the cDNA was treated with Mung bean nuclease (Life Technologies, Gaithersburg, MD), blunt-ended with T4 DNA polymerase (Boehringer  
30    Mannheim, Indianapolis, IN), and ligated to non-palindromic *BstXI* adaptors (Invitrogen, San Diego, CA), using about 50-fold molar excess of the adaptors. The adapted cDNA

was digested with *Not*I, size-fractionated for 1.2-3.0 kb cDNAs by agarose gel electrophoresis, and ligated into pYES2.0 (Invitrogen, San Diego, CA) cleaved with *Bst*XI/*Not*I. The ligation mixture was transformed into electrocompetent *E. coli* DH10B cells (Life Technologies, Gaithersburg, MD) according to the manufacturer's instructions.

5 The library consisting of  $1 \times 10^6$  independent clones was stored as individual pools (25,000-30,000 colony forming units/pool) in 20% glycerol at -80°C, and as double stranded cDNA and ligation mixture at -20°C.

#### Example 5: Genomic DNA extraction

10 *Aspergillus oryzae* 1568 was grown in 25 ml of 0.5% yeast extract-2% glucose (YEG) medium for 24 hours at 37°C and 250 rpm. Mycelia were then collected by filtration through Miracloth (Calbiochem, La Jolla, CA) and washed once with 25 ml of 10 mM Tris-1 mM EDTA (TE) buffer. Excess buffer was drained from the mycelia preparation which was subsequently frozen in liquid nitrogen. The frozen mycelia  
15 preparation was ground to a fine powder in an electric coffee grinder, and the powder was added to a disposable plastic centrifuge tube containing 20 ml of TE buffer and 5 ml of 20% w/v sodium dodecylsulfate (SDS). The mixture was gently inverted several times to ensure mixing, and extracted twice with an equal volume of phenol:chloroform:isoamyl alcohol (25:24:1 v/v/v). Sodium acetate (3 M solution) was added to the extracted sample  
20 to a final concentration of 0.3 M followed by 2.5 volumes of ice cold ethanol to precipitate the DNA. The tube was centrifuged at 15,000 x g for 30 minutes to pellet the DNA. The DNA pellet was allowed to air-dry for 30 minutes before resuspension in 0.5 ml of TE buffer. DNase-free ribonuclease A was added to the resuspended DNA pellet to a concentration of 100 µg per ml and the mixture was then incubated at 37°C for 30 minutes.  
25 Proteinase K (200 µg/ml) was added and the tube was incubated an additional one hour at 37°C. Finally, the sample was extracted twice with phenol:chloroform:isoamyl alcohol and the DNA precipitated with ethanol. The precipitated DNA was washed with 70% ethanol, dried under vacuum, resuspended in TE buffer, and stored at 4°C.

#### 30 Example 6: PCR amplification of *Aspergillus oryzae* 1568 aminopeptidase II

Based on the amino acid sequences of the *Aspergillus oryzae* 1568 aminopeptidase II partial peptides described in Example 2, the degenerate oligonucleotide primers shown

below were synthesized with an Applied Biosystems Model 394 DNA/RNA Synthesizer, according to the manufacturer's instructions, to PCR amplify aminopeptidase II gene fragments from *Aspergillus oryzae* 1568 genomic DNA.

Forward primer: 5'-CCIGAYGARTTYCCIGARGA-3' (SEQ ID NO:3)

5 Reverse primer: 5'-RTTYTTIACIACIGCIACRTCIGCIGTLACYTCLAC-3' (SEQ ID NO:4)

(R= A or G, Y= C or T, N= G or A or C or T, H= A or C or T, I= Inosine) -

Amplification reactions (50  $\mu$ l) were prepared using approximately 1  $\mu$ g of *Aspergillus oryzae* 1568 genomic DNA, prepared as described in Example 5, as the  
10 template. Each reaction contained the following components: 1  $\mu$ g of genomic DNA, 40 pmol of the forward primer, 40 pmol of the reverse primer, 200  $\mu$ M each of dATP, dCTP, dGTP, and dTTP, 1 x *Taq* polymerase buffer (Perkin-Elmer Corp., Branchburg, NJ), and 2.5 Units of *Taq* polymerase (Perkin-Elmer Corp., Branchburg, NJ). The reactions were incubated in a Perkin-Elmer Model 480 Thermal Cycler programmed as follows: Cycle 1  
15 at 94°C for 5 minutes, 50°C for 2 minutes, and 72°C for 2 minutes; and Cycles 2-26 at 94°C for 2 minutes, 50°C for 1 minute, and 72°C for 2 minutes. The reaction products were isolated on a 1.5% agarose gel (Eastman Kodak, Rochester, NY) where a 309 bp product band was excised from the gel and purified using Qiaex II (Qiagen, Chatsworth, CA) according to the manufacturer's instructions. The purified PCR product was  
20 subsequently cloned into a pCRII vector (Invitrogen, San Diego, CA) and the DNA sequence was determined using lac forward and reverse primers (New England BioLabs, Beverly, MA).

The aminopeptidase II gene segment (309 bp) consisting of 103 codons was amplified from *Aspergillus oryzae* 1568 with the aminopeptidase II-specific PCR primers  
25 described above. DNA sequence analysis showed that the amplified gene segment encoded a portion of the corresponding *Aspergillus oryzae* 1568 aminopeptidase II gene. The aminopeptidase II gene segment was used to probe the *Aspergillus oryzae* 1568 cDNA library described in Example 5.

#### 30 Example 7: Identification of *Aspergillus oryzae* 1568 aminopeptidase II clones

The *Aspergillus oryzae* 1568 cDNA library was plated on Luria plus 50  $\mu$ g/ml carbenicillin agar plates. Colony lifts (Maniatis *et al.*, 1982, *Molecular Cloning*, A

*Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, New York) were performed on approximately 10,000 colonies and the DNA was cross-linked onto membranes (Hybond N+, Amersham, Arlington Heights, IL) using a UV Stratalinker (Stratagene, La Jolla, CA). The membranes were soaked for three hours at 45°C in a hybridization solution containing 5 x SSPE, 0.3% SDS, 50% formamide, and 10 µg/ml of denatured and sheared herring sperm DNA. The aminopeptidase II gene fragment isolated from the *Aspergillus oryzae* 1568 as described in Example 6 was radiolabeled using the Random Primed DNA Labeling Kit (Boehringer Mannheim, Mannheim, Germany), denatured by adding NaOH to a final concentration of 0.1M, and added to the hybridization solution at an activity of approximately 1 x 10<sup>6</sup> cpm per ml of hybridization solution. The mixture was incubated overnight at 45°C in a shaking water bath. Following incubation, the membranes were washed three times in 2 x SSC with 0.2% SDS at 55°C. The membranes were then dried on blotting paper for 15 minutes, wrapped in SaranWrap™, and exposed to X-ray film for 48 hours at -70°C with intensifying screens (Kodak, Rochester, NY).

Eleven colonies, produced strong hybridization signals with the probe. The eleven colonies were inoculated into five ml of LB plus 50 µg/ml carbenicillin medium and grown overnight at 37°C. Miniprep DNA was prepared from each of these clones using the Wizard 373 DNA Purification Kit (Promega, Madison, WI). Clone 9 and clone 10 contained aminopeptidase II encoding sequence, as confirmed by DNA sequencing. Clone 9 (pEJG18) was full length. The plasmid pEJG18 was subcloned in *E. coli* DH5α cells to produce *E. coli* DH5α EJG18.

#### **Example 8: DNA sequence analysis of *Aspergillus oryzae* 1568 aminopeptidase II gene**

DNA sequencing of the aminopeptidase II gene contained in pEJG18 in *E. coli* DH5α EJG18 described in Example 7 was performed with an Applied Biosystems Model 373A Automated DNA Sequencer (Applied Biosystems, Inc., Foster City, CA) on both strands using the primer walking technique with dye-terminator chemistry (Giesecke *et al.*, 1992, *Journal of Virology Methods* 38: 47-60). Oligonucleotide sequencing primers were designed to complementary sequences in the aminopeptidase II gene and were synthesized

on an Applied Biosystems Model 394 DNA/RNA Synthesizer according to the manufacturer's instructions.

The nucleotide sequence of the gene encoding the *Aspergillus oryzae* 1568 aminopeptidase II and the deduced amino acid sequence thereof is shown in Figure 1 (SEQ ID NOS:1 and 2, respectively). Sequence analysis of the cloned insert revealed a large open reading frame of 1488 nucleotides (excluding the stop codon) encoding a protein of 496 amino acids sequence (SEQ ID NO:2). The G+C content of this open reading frame is 58%. Based on the rules of van Heijne (van Heijne, 1984, *Journal of Molecular Biology* 173: 243-251), the first 15 amino acids likely comprise a secretory signal peptide which directs the nascent polypeptide into the endoplasmic reticulum (double underlined in Figure 1).

The amino acid sequences of the partial peptides derived from the purified aminopeptidase II as described in Example 2 are underlined in Figure 1 and were consistent with those found in the deduced amino acid sequence (SEQ ID NO:2) of the *Aspergillus oryzae* 1568 aminopeptidase II cDNA.

Using the Clustal alignment program (Higgins, 1989, *supra*) to compare the deduced amino acid sequence of the *Aspergillus oryzae* 1568 aminopeptidase II to that of the *Saccharomyces cerevisiae* aminopeptidase II Y (SEQ ID NO:5), a 33.7% identity was observed.

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**Example 9: Construction of an *Aspergillus oryzae* 1568 aminopeptidase II expression vector for an *Aspergillus* host**

Two synthetic oligonucleotide primers shown below were designed to PCR amplify the *Aspergillus oryzae* A1568 aminopeptidase II gene coding sequence from plasmid pEJG18 (*E. coli* DH5 $\alpha$ -EJG18) for subcloning and expression in an *Aspergillus* host.

Forward primer: 5'-ATGATGAGGTCGCTTTTGTGGGC-3' (SEQ ID NO:6)

Reverse primer: 5'-GGGATGCATCTATGCCTCGACTT-3' (SEQ ID NO:7)

Bold letters represent coding sequence.

In order to facilitate the subcloning of the gene fragment into an expression vector designated pMWR3 (Figure 2), a *Nsi*I restriction enzyme site was introduced at the 3' end of the aminopeptidase II gene. The 5' end was left blunt with an addition of ATG for insertion into the *Swa*I site. The vector pMWR3 contained the TAKA promoter and

30

terminator as regulatory sequences. Since the plasmid does not contain a selectable marker for fungal transformations, it was cotransformed with pToC90 (WO 91/17243) which contains *amdS* as the selectable marker.

Fifty picomoles of each of the primers above were used in a PCR reaction (50  $\mu$ l) containing 70 ng of pEJG18 (an *Aspergillus oryzae* 1568 cDNA clone in pYES2), 1X *Pwo* Buffer (Boehringer Mannheim, Indianapolis, IN), 8  $\mu$ l of a 10 mM blend of dATP, dTTP, dGTP, and dCTP, and 2.5 units of *Pwo*I (Boehringer Mannheim, Indianapolis, IN). The amplification conditions were one cycle at 94°C for 2 minutes, 55°C for 30 seconds, and 72°C for 1 minute; 9 cycles at 94°C for 15 seconds, 55°C for 30 seconds, and 72°C for 1 minutes; 15 cycles at 94°C for 15 seconds, 55°C for 30 seconds, and 72°C for 1 minute, with an extension of 20 seconds per cycle; and a final cycle of 94°C for 15 seconds, 55°C for 30 seconds, and 72°C for 7 minutes. The heat block then went to a 4°C soak cycle. The amplified 1500 bp DNA fragment was purified by gel electrophoresis and Qiaex II. The aminopeptidase clone was digested with *Nsi*I (using conditions specified by the manufacturer). The fragment was phenol-chloroform extracted and ethanol precipitated. The cut fragment was cloned into pMWR3 that had been previously cut with *Swa*I and *Nsi*I resulting in the expression plasmid pEJG19 (Figure 3) in which transcription of the aminopeptidase II gene was under the control of the TAKA promoter. The plasmid pEJG19 was transformed into *E. coli* DH5 $\alpha$  cells (Life Technologies, Gaithersburg, MD). An *E. coli* transformant containing the pEJG19 plasmid was isolated and plasmid DNA was prepared according to procedures described by Sambrook *et al.*, 1989, *supra*.

**Example 10: Expression of the *Aspergillus oryzae* 1568 aminopeptidase II gene in *Aspergillus oryzae***

Plasmid pEJG19 was introduced into an alkaline protease-deficient *Aspergillus oryzae* host JaL142-6 using the following protoplast transformation methods. The transformation was conducted with protoplasts at a concentration of ca.  $2 \times 10^7$  protoplasts per ml. One hundred  $\mu$ l of protoplasts were placed on ice with ca. 5  $\mu$ g of pEJG19 and 5  $\mu$ g of pTOC90; 250  $\mu$ l of 60% PEG 4000, 10 mM Tris-HCl, pH 7.5, 10 mM CaCl<sub>2</sub> was added, and the protoplasts were incubated at 37°C for 30 minutes. Three mls of STC (1.2 M Sorbitol, 10 mM Tris-HCl, pH 7.5, and 10 mM CaCl<sub>2</sub>) was added. The solution was

mixed gently and poured onto COVE transformation plates (per liter: 0.52 g of KCl, 0.52 g of  $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ , 1.52 g of  $\text{KH}_2\text{PO}_4$ , 1 ml of trace metals described below, 342.3 g of sucrose, 25 g of Noble agar, 10 ml of 1 M acetamide, 10 ml of 3 M CsCl). The trace metals solution (1000X) was comprised of 22 g of  $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$ , 11 g of  $\text{H}_3\text{BO}_3$ , 5 g of  $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$ , 5 g of  $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ , 1.6 g of  $\text{CoCl}_2 \cdot 5\text{H}_2\text{O}$ , 1.6 g of  $(\text{NH}_4)_6\text{Mo}_7\text{O}_{24}$ , and 50 g of  $\text{Na}_4\text{EDTA}$  per liter. Plates were incubated 7 days at 37°C. Transformants were transferred to plates of the same medium and incubated 2 days at 37°C. Totally, 140 transformants were recovered by their ability to grow on COVE medium using acetamide as sole nitrogen source.

The transformants were grown for 4 days at 34°C, 200 rpm in 24 well plates containing 1 ml per well of 25% MY50 medium diluted with 75% MY50 salts. MY50 was composed per liter of 50 g of maltodextrin, 2.0 g of  $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ , 10 g of  $\text{KH}_2\text{PO}_4$ , 2 g of citric acid, 10 g of yeast extract, 2.0 g of urea, 2 g of  $\text{K}_2\text{SO}_4$  and 0.5 ml of trace elements solution adjusted to pH 6.0. The trace metals solution was composed per liter of 14.3 g of  $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$ , 2.5g of  $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ , 0.5g of  $\text{NiCl}_2 \cdot 6\text{H}_2\text{O}$ , 13.8 g of  $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ , 8.5 g of  $\text{MnSO}_4 \cdot \text{H}_2\text{O}$ , 3 g of citric acid. The MY50 salts was composed per liter of 2.0 g of  $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ , 10 g of  $\text{KH}_2\text{PO}_4$ , 2 g of citric acid, and 2 g of  $\text{K}_2\text{SO}_4$ , pH 6.0.

Each of the 140 wells were assayed for aminopeptidase II activity using Leu-pNA (hydrochloride salt) as substrate. In a 96 well microtiter plate, 4  $\mu\text{l}$  of supernatant was added to 100  $\mu\text{l}$  of 1 mg/ml of Leu-pNA in 50 mM sodium phosphate pH 7.5 buffer. The absorbance at 405 nm was monitored.

Four transformants, 20, 88, 90, and 137, with the highest level of aminopeptidase II activity were then grown in 125 ml shake flasks for 4 days at 34°C containing 25 ml of MY50 medium.

Samples were assayed on day 2, 3, and 4 for aminopeptidase II activity by mixing 100  $\mu\text{l}$  of 10-fold diluted supernatant with 100  $\mu\text{l}$  of 2 mg/ml Leu-pNA in 50 mM sodium phosphate pH 7.5 buffer. Transformants 20, 90, and 137 were the highest producers. For purification of the aminopeptidase II, transformants 20 and/or 90 were grown in shake flasks as above or in a fermentation medium composed of suitable carbon and nitrogen sources.

**Example 11: Purification of recombinant *Aspergillus oryzae* 1568 aminopeptidase II produced in *Aspergillus***

The combined supernatants from the shake flask broths described in Example 10 were combined (approximately 100 mg of protein in approximately 100 ml) and was diluted to 3.7 mS and adjusted to pH 7.0. The diluted sample was then loaded onto Q-Sepharose, Big Beads, pre-equilibrated with 20 mM sodium phosphate pH 7.0 buffer. The aminopeptidase II was eluted with a 0-0.4 M NaCl gradient in 20 mM sodium phosphate pH 7.0 buffer followed by a wash with 0.4 M NaCl. Fractions were assayed for aminopeptidase II activity by mixing 100  $\mu$ l of each fraction with 100  $\mu$ l of 2 mg of Leu-pNA per ml of 50 mM sodium phosphate pH 7.5 buffer. The assay results indicated that the aminopeptidase II eluted at the end of the gradient and during the 0.4 M NaCl wash. Analysis by SDS-PAGE revealed that the enzyme was homogeneous.

**Example 12: Construction of an *Aspergillus oryzae* 1568 aminopeptidase II expression vector for a *Fusarium* host**

Two synthetic oligonucleotide primers shown below were designed to PCR amplify the *Aspergillus oryzae* A1568 aminopeptidase II gene coding sequence from plasmid pEJG18 (*E. coli* DH5 $\alpha$ -EJG18) for subcloning and expression in a *Fusarium* host.

Forward primer: 5'-ATTTAAATcaccATGAGGTCGCTTTTGTGGGC-3' (SEQ ID NO:8)

Reverse primer: 5'-GGGTTAATTAAGTATGCCTCGACTTGAGAATG-3' (SEQ ID NO:9)

Bold letters represent coding sequence. Small case represents a Kozak consensus sequence to enhance expression (Kozak, 1981, *Nucleic Acids Research* 12. 857-872).

In order to facilitate the subcloning of the gene fragment into an expression vector designated pDM181 (Figure 4), *Swa*I and *Pac*I restriction enzyme sites were introduced at the 5' and 3' end of the aminopeptidase II gene, respectively. The vector pDM181 contained the *Fusarium oxysporum* trypsin-like protease (SP387) promoter and terminator (WO 96/00787) as regulatory sequences. The plasmid also contained the *bar* gene as a selectable marker for fungal transformations (de Block *et al.*, 1987, *EMBO Journal* 6:2513-2518).

Fifty picomoles of each of the primers above were used in a PCR reaction containing 70 ng of pEJG18, 1X *Pwo* Buffer, 5 µl of 10 mM blend of dATP, dTTP, dGTP, and dCTP, and 2.5 units of *Pwo*I. The amplification conditions were one cycle at 94°C for 2 minutes, 55°C for 30 seconds, and 72°C for 1 minute; 9 cycles each at 94°C for 15 seconds, 55°C for 30 seconds, and 72°C for 1 minute; 15 cycles each at 94°C for 15 seconds, 55°C for 30 seconds, and 72°C for 1 minute, with an extension of 20 seconds per cycle; and a final cycle at 94°C for 15 seconds, 55°C for 30 seconds, and 72°C for 7 minutes. The heat block was then held at a 4°C soak cycle. The amplified 1500 bp DNA fragment was purified by gel electrophoresis and Qiaex II, and then subcloned into pCRII TOPO TA cloning vector (Stratagene, San Diego, CA). The pCRII aminopeptidase clone was cut with restriction endonucleases *Swa*I and *Pac*I (using conditions specified by the manufacturer). The fragment was purified by gel electrophoresis and Qiaex II. The cut fragment was cloned into pDM181 that had been previously cut with *Swa*I and *Pac*I resulting in the expression plasmid pEJG28 (Figure 5) in which transcription of the aminopeptidase II gene was under the control of the *Fusarium oxysporum* trypsin-like protease promoter. The plasmid pEJG28 was transformed into *E. coli* ABLE K cells (Stratagene, San Diego, CA). The *E. coli* transformant containing the pEJG28 plasmid was isolated and plasmid DNA was prepared according to procedures described by Sambrook *et al.*, 1989, *supra*.

#### Example 13: Transformation of *Fusarium* CC1-3 and analysis of transformants

*Fusarium* strain CC1-3, a highly branched morphological mutant of *Fusarium* strain A3/5 (ATCC 20334) (Wiebe *et al.*, 1992, *Mycological Research* 96: 555-562; Wiebe *et al.*, 1991, *Mycological Research* 95: 1284-1288; Wiebe *et al.*, 1991, *Mycological Research* 96: 555-562), was grown in a liquid medium containing Vogel's salts (Vogel, 1964, *Am. Nature* 98: 435-446), 25 mM NaNO<sub>3</sub>, and 1.5% glucose for 4 days at 28°C and 150 rpm. Conidia were purified by filtration through 4 layers of cheesecloth and finally through one layer of Miracloth. Conidial suspensions were concentrated by centrifugation. Fifty ml of YPG medium comprised of 1% yeast extract, 2% bactopectone, and 2% glucose were inoculated with approximately 10<sup>8</sup> conidia, and incubated for 14 hours at 24°C and 150 rpm. Resulting hyphae were trapped on a sterile 0.4 mm filter and washed successively with sterile distilled water and 1.0 M MgSO<sub>4</sub>. The hyphae were resuspended in 10 ml of

NOVOZYM 234™ solution (2-10 mg/ml in 1.0 M MgSO<sub>4</sub>) and digested for 15-30 minutes at 34°C with agitation at 80 rpm. NOVOZYM 234™ was obtained from Novo Nordisk A/S, Bagsværd, Denmark. Undigested hyphal material was removed from the resulting protoplast suspension by successive filtration through 4 layers of cheesecloth and through  
5 Miracloth. Twenty ml of 1 M sorbitol were combined with the protoplast solution. After mixing, the protoplasts were pelleted by centrifugation and washed successively by resuspension and centrifugation in 20 ml of 1 M sorbitol and in 20 ml of STC (0.8-M sorbitol, 0.05 M Tris pH 8.0, 0.05 M CaCl<sub>2</sub>). The washed protoplasts were resuspended in 4 parts STC and 1 part SPTC (0.8 M sorbitol, 40% PEG 4000, 0.05 M Tris pH 8.0, 0.05  
10 M CaCl<sub>2</sub>) at a concentration of  $5 \times 10^7$ /ml.

One hundred ml of protoplast suspension were added to 10 µg of pEJG28 in polypropylene tubes (17 x 100 mm), mixed and incubated on ice for 30 minutes. One ml of SPTC was mixed gently into the protoplast suspension and incubation was continued at room temperature for 20 minutes. 12.5 ml of molten solution (cooled to 40°C) consisting  
15 of 1X Vogel's salts, 25 mM NaNO<sub>3</sub>, 0.8 M sucrose and 1% low melting agarose (Sigma Chemical Company, St. Louis, MO) were mixed with the protoplasts and then plated onto an empty 100 mm Petri plate. Incubation was continued at room temperature for 10 to 14 days. After incubation at room temperature for 24 hours, 12.5 ml of the identical medium plus 10 mg of BASTA™ (Hoechst Schering, Rodovre, Denmark) per ml were overlayed  
20 onto the Petri plate. BASTA™ was extracted twice with phenol:chloroform:isoamyl alcohol (25:24:1), and once with chloroform:isoamyl alcohol (24:1) before use.

After two weeks, 2 transformants designated #1 and #2 were apparent. A mycelial fragment from the edge of each transformant was transferred to individual wells of a 24 well plate containing Vogel's/ BASTA™ medium. The medium contained 25 g of sucrose,  
25 25 g of Noble agar, 20 ml of 50X Vogel's salts (Vogel, 1964, *supra*), 25 mM NaNO<sub>3</sub>, and 10 g of BASTA™ per liter. The plate was sealed in a plastic bag to maintain moisture and incubated approximately one week at room temperature.

**Example 14: Expression of *Aspergillus oryzae* 1568 aminopeptidase II gene in  
30 *Fusarium***

A mycelial fragment from each of the 2 *Fusarium* CC1-3 transformants described in Example 13 was inoculated into 20 ml of M400Da medium composed of 50 g of maltodextrin, 2.0 g of  $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ , 2.0 g of  $\text{KH}_2\text{PO}_4$ , 4.0 g of citric acid, 8.0 g of yeast extract, 2.0 g of urea, and 0.5 ml of trace metals solution per liter and incubated for 7 days at 30°C and 150 rpm. The medium was adjusted to pH 6.0 with 5 N NaOH. The trace metals solution contained 14.3 g of  $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$ , 2.5 g of  $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ , 0.5 g of  $\text{NiCl}_2 \cdot 6\text{H}_2\text{O}$ , 13.8 g of  $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ , 8.5 g of  $\text{MnSO}_4 \cdot \text{H}_2\text{O}$ , and 3.0 g of citric acid per liter. The untransformed host was also run as a control. One ml of culture supernatant was harvested at 7 days and stored and assayed. Amino peptidase II activity was determined by mixing 10 µl of supernatant with 200 µl of a substrate stock solution containing 2 mg of Leu-para-nitroanilide per ml of 50 mM sodium phosphate pH 7.5 buffer and monitoring the change in absorbance at 405 nm over 4 minutes. Both transformants exhibited activity towards Leu-pNA greater than the untransformed control.

The primary *Fusarium* transformant #2 described in Example 13 was cultivated in 125 ml shake flasks for 5 days at 30°C in 25 ml of M400Da medium. The whole culture broth was filtered using a double layer of Miracloth. The filtrate was recovered and then frozen at -20°C.

**Example 15: Purification of recombinant *Aspergillus oryzae* 1568 amino peptidase II produced by *Fusarium***

A 20 ml volume of a 5 day *Fusarium* broth described in Example 14 was filtered through a 0.45 micron syringe filter. The sample was then diluted 8-fold in 20 mM sodium phosphate buffer pH 7.0 buffer. The conductivity and pH of the sample was 3.1 mS and 7.10, respectively. The sample was loaded onto a XK-26 (Pharmacia Biotech AB, Uppsala, Sweden) column containing 60 ml of Q-Sepharose, Big Beads, which had been pre-equilibrated with 20 mM sodium phosphate pH 7.0 buffer. The column was washed until a baseline was reached and then the sample was eluted with a linear gradient from 0-0.5 M NaCl in 20 mM sodium phosphate buffer pH 7.0 over 8.3 column volumes and at a flow rate of 5 ml/min. Fractions were assayed using Leu-pNA as substrate by mixing 10 µl of each fraction with 90 µl of 50 mM sodium phosphate pH 7.5 buffer and 100 µl of a substrate stock solution containing 2 mg of Leu-pNA per ml of 50 mM sodium phosphate

pH 7.5 buffer and monitoring the change in absorbance at 405 nm over 4 minutes. All fractions active on Leu-pNA were then pooled, diluted, and concentrated using an Amicon Ultrafiltration unit utilizing a PM 10 membrane.

The concentrated sample was then loaded onto a Mono Q 16/10 (Pharmacia Biotech AB, Uppsala, Sweden) column which had been pre-equilibrated with 20 mM sodium phosphate pH 7.0 buffer. The column was then washed with 0.15 M NaCl. A gradient was performed from 0.15-0.5 M NaCl over 10 column volumes at a flow rate of 2 ml/min. Active fractions were then equilibrated in 1.7 M  $(\text{NH}_4)_2\text{SO}_4$  in 50 mM sodium phosphate buffer pH 7.0.

The sample was then loaded onto a Phenyl Superose 5/5 column (Pharmacia Biotech AB, Uppsala, Sweden) which had been pre-equilibrated with 1.7 M  $(\text{NH}_4)_2\text{SO}_4$  in 50 mM sodium phosphate pH 7.0 buffer. The column was washed with 1.7 M  $(\text{NH}_4)_2\text{SO}_4$  in 50 mM sodium phosphate pH 7.0 buffer until baseline was achieved. The enzyme was eluted with a gradient from 1.7 M to 0 M  $(\text{NH}_4)_2\text{SO}_4$  over 30 column volumes at a flow rate of 0.5 ml/min. The flow through had activity on Leu-pNA, as did fractions that were eluted. The enzyme appeared as a series of differentially glycosylated forms based on SDS-PAGE analysis. When the various forms of the enzyme were treated with Endoglycosidase F/N glycosidase F (Boehringer Mannheim, Indianapolis, IN), according to the manufacturer's suggested protocol, a single band with a molecular weight of ~58 kDa appeared in all the samples analyzed. The differentially glycosylated forms were then pooled, desalted using 50 mM sodium phosphate buffer pH 7.5, and submitted to biochemical characterization.

#### **Example 16: Characterization of recombinant *Aspergillus oryzae* 1568 aminopeptidase II**

The purified aminopeptidase II described in Example 11 was used in the following characterization.

Kinetic parameters of the aminopeptidase II were determined for several p-nitroanilides (pNA) including Leu-pNA, Gly-pNA, Ala-pNA, and Pro-pNA (Sigma Chemical Co., St. Louis, MO, or Bachem, Torrance, CA). Stock solutions of 100 mg of each p-nitroanilide per ml of dimethylsulfoxide were diluted with 50 mM potassium phosphate pH 7.0 buffer to concentrations ranging from 0.0064 to 9.56 mM. It should be noted that the solubility of the substrates is not always sufficient to have concentrations

comparable to  $K_m$ , which may result in errors which could be higher than expected normally. The reaction of the aminopeptidase II with the p-nitroanilide was initiated when a 100  $\mu$ l aliquot of the enzyme solution in 50 mM potassium phosphate pH 7.0 was added to 100  $\mu$ l of a substrate solution in a microtiter plate well and monitored at 405 nm and 25°C using a THERMOmax Microplate Reader (Molecular Devices Corp., Sunnyvale, CA). Analysis of initial rates of hydrolysis of the p-nitroanilides produced the results shown in Table 1:

Table 1. Kinetic parameters of aminopeptidase II at pH 7.0 and 25°C

Substrate	$K_m$ (mM)	$V_{max}$ (relative units)
Leu-pNA	7	6400
Gly-pNA	0.3	1670
Ala-pNA	11	1200
Pro-pNA	2	120

The results showed that the aminopeptidase II possesses a substrate specificity where the specificity toward Ala is much worse than toward Gly.

Inhibition of the aminopeptidase II with 1,10-phenanthroline was evaluated using Leu-pNA as substrate at pH 7.5 in 50 mM Tris pH 7.5 buffer where hydrolysis was monitored at 405 nm. A 200 mM solution of 1,10-phenanthroline in methanol was prepared. The inhibition reaction was conducted by mixing 100  $\mu$ l of 2 mg of Leu-pNA per ml of 50 mM sodium phosphate pH 7.5 solution and 10  $\mu$ l of the 1,10-phenanthroline solution with 100  $\mu$ l of aminopeptidase II diluted 5-fold in 50 mM sodium phosphate pH 7.5 buffer. A control was run where 10  $\mu$ l of 20 mM Tris pH 7.6 buffer was used in place of the 1,10-phenanthroline solution.

The results indicated that 1,10-phenanthroline inhibited the aminopeptidase II suggesting that the aminopeptidase II is a metalloprotease. The rate of hydrolysis of Leu-pNA decreased from 285 mOD/minute to 21 mOD/minute in the presence of 1,10-phenanthroline.

The purified aminopeptidase II described in Example 15 was used in the following characterizations.

The pH optimum was determined using Ala-pNA as substrate in the universal buffer composed of 0.125 M citric acid, 0.125 M mono basic sodium phosphate, and 0.125 M

boric acid pH was adjusted to 4.5-11 with 10 N NaOH, in 0.5 pH increments. The Ala-pNA substrate was prepared by dissolving 100 mg of Ala-pNA in 1 ml of DMSO and adding 20  $\mu$ l of the Ala-pNA/DMSO solution to 980  $\mu$ l of the universal buffer at the various pH values. The assay was initiated by adding a 15  $\mu$ l aliquot of the aminopeptidase  
 5 II in 50 mM sodium phosphate pH 7.5 buffer to 200  $\mu$ l of 2 mg/ml Ala-pNA at the various pH values at ambient temperature. The change in absorbance at 405 nm was monitored for 5 minutes. Autohydrolysis of the substrate as a control was determined by adding 15  $\mu$ l of 50 mM sodium phosphate pH 7.5 buffer to 200  $\mu$ l of 2 mg/ml Ala-pNA at the various pH values.

10 The results shown in Table 2 below demonstrated that the aminopeptidase II possessed activity with Ala-pNA as substrate over the measured pH range 4.91 to 10.91 with optimal activity at pH ~9.5-10. No autohydrolysis of the substrate was observed at pH values of 11 or less.

Table 2

	pH	Avg. Activity	Relative Activity
15	4.42	0 mOD/min	0
	4.91	2	0.006
	5.41	7.8	0.024
	5.89	13.9	0.043
20	6.40	16.37	0.051
	6.90	23.48	0.0727
	7.27	41.24	0.128
	7.59	69.15	0.214
	8.03	145.6	0.45
25	8.62	245.99	0.761
	9.25	306.97	0.95
	9.68	323.15	1.0
	10.51	270.8	0.838
	10.95	197.86	0.612

30 The temperature stability of the aminopeptidase II was determined using the following protocol: 480  $\mu$ l of 50 mM sodium phosphate buffer pH 7.5 was preincubated at 37°, 45°, 55°, 60°, 65°, 70°, and 75°C for 30 minutes in a 1.7 ml Eppendorf tube. Then

20  $\mu$ l of purified aminopeptidase II was added and the sample was then incubated for an additional 20 minutes. The samples were then placed on ice. Once the incubations were completed for all the temperatures, the samples were then assayed for activity using Leu-pNA as substrate.

5 The assay was performed by mixing 100  $\mu$ l of the incubation mixtures for the various temperatures with 100  $\mu$ l of 2 mg/ml Leu-pNA in 50 mM sodium phosphate pH 7.5 buffer at ambient temperature. The absorbance at 405 nm was monitored for 5 minutes. --

The results shown in Table 3 demonstrated that the aminopeptidase II retained 90% of its activity after a 20 minute incubation at 60°C, pH 7.5.

10 Table 3

Temperature (°C)	Percent activity relative to 37°C
37	100
45	101
55	99
15 60	90
65	73.7
70	64.6
75	46

The kinetic parameters for various aminopeptidase II substrates was determined using the following protocol. Purified aminopeptidase II with an  $A_{280}$  of 0.581 was used. Each substrate was dissolved in DMSO to a concentration of 100 mg/ml and then diluted 50 fold in 50 mM sodium phosphate pH 7.5 buffer to 2 mg/ml. The substrates included Leu-pNA, Glu-pNA (Bachem, Torrance, CA), and Ala-pNA. In a 96 well microtiter plate, 10  $\mu$ l of purified aminopeptidase II was incubated with each substrate as follows except 50  $\mu$ l of purified aminopeptidase II was incubated with Glu-pNA, and the absorbance at 405 nm was measured for 4 minutes:

1. 200  $\mu$ l of 2 mg/ml substrate + 0  $\mu$ l of 50 mM sodium phosphate buffer pH 7.5
2. 100  $\mu$ l of 2 mg/ml substrate + 100  $\mu$ l of 50 mM sodium phosphate buffer pH 7.5
3. 50  $\mu$ l of 2 mg/ml substrate + 150  $\mu$ l of 50 mM sodium phosphate buffer pH 7.5
- 30 4. 25  $\mu$ l of 2 mg/ml substrate + 175  $\mu$ l of 50 mM sodium phosphate buffer pH 7.5

A Lineweaver-Burke plot was constructed to determine the  $K_m$  and the  $k_{cat}$  for each substrate, using an average molecular weight of 97 kDa for the differentially glycosylated forms.

For Leu-pNA, the  $K_m$  and  $k_{cat}$  were determined to be 5.78 mM and 230.9 min<sup>-1</sup>,  
5 respectively.

For Glu-pNA, the  $K_m$  and  $k_{cat}$  were determined to be 1.17 mM and 8.217 min<sup>-1</sup>,  
respectively.

For Ala-pNA, the  $K_m$  and  $k_{cat}$  were determined to be 1.49 mM and 34.638 min<sup>-1</sup>,  
respectively.

10

#### **Example 17: Preparation of protein hydrolysates with *Aspergillus oryzae* 1568 aminopeptidase II**

The purified aminopeptidase II described in Example 11 was tested in degree of hydrolysis assays using soy, wheat gluten, and casein as substrates according to the  
15 following procedure.

The degree of hydrolysis (DH) assays were performed at 50°C for 18 hours as a mini-hydrolysis on a 10 ml scale using soy bean meal tablets, wheat gluten meal tablets, and sodium-caseinate at a 2% concentration adjusted to pH 7, if necessary, with no pH adjustment during hydrolysis. The hydrolysates were inactivated at 85°C for 3 minutes in  
20 a waterbath. The enzymes used were FLAVOURZYME™ and aminopeptidase II. The enzymes were dosed as follows. For soy, 2 LAPUs and 5 LAPUs of aminopeptidase II (recombinant) were added compared to 3 LAPUs of FLAVOURZYME™. For gluten, 2 LAPUs and 5 LAPUs of aminopeptidase II (recombinant) were added compared to 3 LAPUs of FLAVOURZYME™. For casein, 1 and 2 LAPUs of aminopeptidase II  
25 (recombinant) were added compared to 3 LAPUs of FLAVOURZYME™. One LAPU (Leucine Amino Peptidase Unit) is the amount of enzyme which decomposes 1 micromole of L-leucine-p-nitroanilide per minute under the following conditions: 26 mM L-leucine-p-nitroanilide in 0.1 M Tris pH 8.0 buffer at 40°C for 10 minutes. Upon hydrolysis, p-nitroanilide is liberated turning the solution yellow which is monitored 405 nm.

30 The degree of hydrolysis (DH), as defined as described by Adler-Nissen (1986, *Enzymic Hydrolysis of Food Proteins*, Elsevier Applied Science Publishers), was

determined by reaction of the supernatant with OPA (ortho-phthalaldehyde, Sigma Chemical Co., St. Louis, MO) according to the following procedure. The hydrolysate was diluted 100-fold into distilled water. Then 120  $\mu$ l was transferred to 900  $\mu$ l of OPA reagent. For the OPA reagent, 160 mg of OPA was dissolved in 4 ml of ethanol and transferred to a 200 ml volumetric flask containing a solution of 7.62 g of disodium tetraborate decahydrate, 200 mg of sodium dodecylsulphate, and 176 mg of dithiothreitol and the flask was filled to 200 ml with water. The solution was then shaken well and after 2 minutes exactly, the absorbance at 340 nm was measured and compared to the absorbance of a 0.95 mM L-serine (distilled water) solution after subtraction of the blank value (water reacted with OPA reagent). To determine the true DH, the serine equivalents measured in the hydrolysates were corrected with the factors suggested by Adler-Nissen for the trinitrobenzenesulfonic acid method (Adler-Nissen, 1979, *Agricultural and Food Chemistry* 17: 1256) which gave the same response as the described OPA method. The DH was calculated on the basis of the total amount of protein in the hydrolysis mixture (not on the basis of soluble protein).

A volume of 25  $\mu$ l of suitably diluted supernatant was mixed with 200  $\mu$ l of OPA reagent in a microtiter plate well and allowed to react for exactly 2 minutes at 25°C. The absorbance at 340 nm was measured in a microtiter plate reader and compared to the absorbance of a 95 mM L-serine standard solution after subtraction of the blank value (water reacted with OPA-reagent). To determine the true DH, the serine equivalents measured in the supernatants were corrected with the factors suggested by Adler-Nissen for the trinitrobenzenesulfonic acid method (Adler-Nissen, 1979, *Agricultural and Food Chemistry* 17: 1256) which gave the same response as the described OPA method. The degree of hydrolysis was calculated on basis of the total amount of protein in the hydrolysis mixture (not on basis of soluble protein).

For soy, the addition of 2 LAPUs and 5 LAPUs of aminopeptidase II to 3 LAPUs of FLAVOURZYME™ increased absolute DH at least 8% and 10%, respectively, above the samples with 3 LAPUs of FLAVOURZYME™ alone.

For gluten, the addition of 2 LAPUs and 5 LAPUs of aminopeptidase II to 3 LAPUs of FLAVOURZYME™ increased absolute DH 6% and 9%, respectively.

For gelatin, the addition of 2 LAPUs and 5 LAPUs of dipeptide aminopeptidase II to 3 LAPUs of FLAVOURZYME™ increased absolute DH 4.9% and 5.3% respectively.

For casein, the addition of 1 and 2 LAPUs of aminopeptidase II to 3 LAPUs of FLAVOURZYME™ increased absolute DH 7% and 9%, respectively, over the addition of  
5 3 LAPUs of FLAVOURZYME™ alone.

**Example 18: Hydrolysis of soy protein with *Aspergillus oryzae* aminopeptidase II**

Soy protein in the form of defatted soy bean meal was hydrolysed on a 10 ml-scale (mini-hydrolysis) with a start pH of 7.0 and a protein concentration of 2%. The hydrolysis  
10 time and temperature were 18 hours and 50°C, respectively. Enzymes were inactivated at 85°C for 5 minutes and the hydrolysates were centrifuged. The supernatants were analysed for DH using the OPA-method. The DH, as defined as described by Adler-Nissen (1986, *Enzymic Hydrolysis of Food Proteins*, Elsevier Applied Science Publishers), was determined by reaction of the supernatant with OPA (ortho-phthaldialdehyde, Sigma  
15 Chemical Co., St. Louis, MO) according to Church *et al.*, 1983, *Journal of Dairy Science* 66: 1219-1227. For the OPA reagent, 160 mg of OPA was dissolved in 4 ml of ethanol and transferred to a 200 ml volumetric flask containing a solution of 7.62 g of disodium tetraborate decahydrate, 200 mg of sodium dodecylsulphate, and 176 mg of dithiothreitol and the flask was filled to 200 ml with water. Selected samples were analysed for the  
20 content of free amino acids using the PicoTag HPLC method (Waters Associates, Milford, MA) according to the manufacturer's instructions.

The dosages of enzymes to each hydrolysis flask containing 200 mg of soy protein are shown in Table 4 below. The dosage of FLAVOURZYME™ 1000L was in percent of the soy protein substrate such that 1.5% FLAVOURZYME™ 1000L equals 3 mg of  
25 FLAVOURZYME™ 1000L added to 200 mg of soy protein. In addition to FLAVOURZYME™ 1000L, 1.5% ALCALASE® 2.4L was added to all hydrolysis flasks which equals 3 mg per 200 mg of soy protein. The aminopeptidase II was produced recombinantly in *Aspergillus oryzae* as described in Example 10 and purified accordingly. The aminopeptidase II solution had an A<sub>280</sub> of 8.1 and an estimated protein content of 5  
30 mg/ml from amino acid determination.

The results of the DH analysis are presented in Table 4. DH was calculated from the total protein concentration of 2% - not the soluble protein content.

Table 4. The DH results for the hydrolysates

	FLAVOURZYME™ 1000L (%)	Aminopeptidase II (g enzyme protein/kg soy protein)*	DH (%)
1	1.5	0	45.1
2	1.5	0.03	50.9
3	1.5	0.06	51.0
4	1.5	0.12	51.3
5	1.5	0.25	55.7
6	1.5	0.50	58.0
7	2.0	0	51.9
8	6.0	0	62.8
9	6.0	0.03	62.9
10	6.0	0.06	62.9
11	6.0	0.12	63.6
12	6.0	0.25	68.5
13	6.0	0.50	67.8
14	7.0	0	63.2

\* The concentration of aminopeptidase II used for this calculation is 5 mg/ml

Table 5 shows the relative % increase in the individual free amino acids upon addition of a maximal aminopeptidase II dosage (0.5 g per kg soy protein) to a background dosage of FLAVOURZYME™ and 1.5% ALCALASE® 2.4L. The increase was measured relative to the release of free amino acids resulting from the background enzyme dosages.

Table 5. Relative increase in free amino acids due to addition of aminopeptidase II

Amino acid	1.5% FLAVOURZYME™ + Aminopeptidase II	6% FLAVOURZYME™ + Aminopeptidase II
Asp	123.4	26.0
Glu	54.2	24.5
Asn	115.1	-7.0

	Ser	123.8	0.0
	Gln	91.7	19.8
	Gly	145.7	22.4
	His	31.9	2.8
5	Arg	24.9	6.1
	Thr	40.4	8.8
	Ala	77.4	18.5
	Aro	87.5	59.2
	Tyr	51.3	10.5
10	Val	41.4	12.7
	Met	36.8	9.7
	Cys	74.4	23.2
	Ile	24.6	13.0
	Leu	22.4	7.5
15	Phe	22.8	8.0
	Lys	49.0	10.3
	total	49.1	10.6
	DH	28.7	8.0

20 The results showed that when aminopeptidase II was added to a low dosage of FLAVOURZYME™ (1.5%) plus 1.5% ALCALASE® 2.4L, Gly showed the highest relative % increase followed by Ser, Asp, Asn, Pro, Cys, and Ala. When aminopeptidase II was added to a high FLAVOURZYME™ dosage (6%) plus 1.5% ALCALASE® 2.4L, Pro showed the highest relative % increase followed by Asp, Glu, Cys, Gly, and Gln.

#### 25 **Example 19: Increased protein solubility and release of glutamate by deamidation**

Wheat gluten (WG) was obtained from Cargill (JOB 5141) and deamidated wheat gluten (DWG) was obtained from StaPro Consultancy B.V., Lemdijk 32, 9422 TH Smilde, NL. Suspensions of 8% protein were made by mixing 11 g of gluten with 89 g of water. The pH was adjusted to 6.5 with NaOH. Glutamate/aspartate specific protease (SP446), 30 obtainable as described in WO 91/13554, or lysine/arginine specific protease (SP387) obtainable as described in WO 89/06270, was added to the suspensions. The dosage was

0.01 AU/g protein for SP446 and 0.006 AU/g protein for SP387. FLAVOURZYME™ (an un-specifically acting protease preparation available from Novo Nordisk A/S, Bagsværd, Denmark, containing endo- and exo-peptidase activities, and obtained by fermentation of *Aspergillus oryzae*) was added to some of the hydrolysates at a dosage of 20 LAPU/g protein.

The hydrolyses were carried out at 50°C without further pH adjustment for 18 hours. The enzymes were inactivated by heating at 85°C for 15 minutes. The pH was adjusted to 5 and the hydrolysates were centrifuged. The content of protein and free glutamate in the supernatant was determined.

The protein content was determined by Kjeldahl analysis, using a Kjeldahl factor of 6.25.

The content of free glutamate was determined by use of a glutamate determination kit according to the manufacturer's instructions (Boehringer-Mannheim, Indianapolis, IN). The method was adapted for use in microtiter plates.

When comparing wheat gluten (WG) to deamidated wheat gluten (DWG), the results shown in Table 6 demonstrated that deamidation increased the susceptibility of the gluten to specific proteases, such that more protein became soluble. By addition of FLAVOURZYME™ with a specific protease, the release of glutamate was doubled due to deamidation.

Table 6

Hydrolysate	Protein Solubility - %		Glutamate Content (mg/l)	
	WG	DWG	WG	DWG
SP446	18	54	0	0
SP387	35	44	0	0
SP446 + FLAVOURZYME™	34	87	1000	2000

#### Example 20: Enzymatic deamidation and release of glutamate

Peptidoglutaminase II was produced by growing *Bacillus circulans* strain ATCC 21590 in shake flasks (400 ml) containing 200 ml of a medium composed of 1% polypeptone, 0.5% lactose, 0.025%  $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ , 0.005%  $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ , 0.025%  $\text{KH}_2\text{PO}_4$ , and 17%  $\text{Na}_2\text{HPO}_4 \cdot 12\text{H}_2\text{O}$  (pH adjusted to 7.2), at 30°C for 20 hours with mixing at 270

rpm. The cells were harvested by centrifugation at 4000 rpm in 1 litre flasks. The cells were then frozen.

The purification of peptidoglutaminase II from *Bacillus circulans* was performed at room temperature. The frozen *Bacillus circulans* cells were thawed and suspended in Lysis buffer (50 mM Tris/HCl; 25% (w/v) sucrose; 1 mM EDTA, pH 8.0) until a homogeneous suspension was obtained - 100 g wet cells per liter of Lysis buffer. Lysozyme (10 mg/ml) and DNase I (Sigma DN-25, 10 mg/ml) were dissolved in Lysis buffer. Then 100 ml-of lysozyme solution, 10 ml of 1.0 M  $MgCl_2$ , and 1 ml of DNase I solution were added per litre of cell suspension. The enzymes were allowed to act for 1 hour.

The suspension was filtered through a Seitz depth filter plate and the filtrate was transferred to a 10 mM  $KH_2PO_4/NaOH$ , pH 8.0 (Buffer A) on a Sephadex G25 column (Pharmacia Biotech AB, Uppsala, Sweden). The enzyme solution was applied to a SOURCE Q column (Pharmacia Biotech AB, Uppsala, Sweden) equilibrated in Buffer A and eluted with a linear NaCl gradient (0 → 500 mM) in Buffer A. Fractions from the column were analysed for peptidoglutaminase II activity as described below and fractions with activity were pooled. The absorbance of the pooled fractions at 280 nm was 1.78, thus the protein content was estimated to 1.8 mg/ml.

The purity of the protein in the peptidoglutaminase II pool was approximately 25% as judged from a SDS-PAGE gel. Thus, the preparation contained approximately 0.5 mg/ml of pure peptidoglutaminase II.

The peptidoglutaminase activity was determined by measuring the ammonia formed during hydrolysis of  $\gamma$ -carboxyamide of N-tert-Butoxycarbonyl-Gln-Pro (N-t-BOC-Gln-Pro; SIGMA No. B-4403) using the Boehringer-Mannheim kit for ammonia determination (Cat. No. 1112732). In this kit, ammonia is measured by determination of the consumption of NADH by glutamate dehydrogenase, and blanks without the addition of N-t-BOC-Gln-Pro were also applied in order to subtract the effect of other NADH consuming enzymes.

A total of 200 mg of wheat gluten protein was added to 9 ml of boiling water and after cooling, the pH was adjusted to 7.0. Then 250  $\mu$ l of the peptidoglutaminase II preparation (PEP) described above was added. The glutamate/aspartate specific protease (SP446) described in Example 19 was added in an amount of 0.04 AU/g protein, and

FLAVOURZYME™ described in Example 19 was added in an amount of 20 LAPU/g protein.

Hydrolysis was allowed to proceed without pH adjustment for 18 hours at 50°C. Controls without the addition of peptidoglutaminase were also run. The hydrolysates were centrifuged and glutamate was measured as described in Example 19. The DH was determined as described in Example 18.

The results as shown below in Table 7 demonstrated that hydrolysis with the peptidoglutaminase preparation increased the DH as well as the release of glutamate.

Table 7

Hydrolysis	DH %	Glutamate (mg/l)
Minus PEP	40	131
Plus PEP	43	171

**Example 21: Production of crude enzyme extract powder from *Spingomonas capsulata***

*Sphingomonas capsulata* IFO 12533 was cultivated at 30°C for 9 hours with aeration and agitation in a 5 liter fermentor containing 3 liters of medium composed of 0.5% sucrose, 1% gelatin, 0.5% yeast extract, 1% corn steep liquor, 0.3% sodium chloride, 0.2% dipotassium hydrogen phosphate, and 0.1% magnesium sulfate-7H<sub>2</sub>O. The cell mass was collected from the culture broth and washed twice in 10 mM Tris-HCl pH 8.0 buffer yielding 43 g wet weight of cell mass. The cell mass was suspended in 200 ml of 10 mM Tris-HCl pH 8.0 buffer and lysed by adding lysozyme and Triton X-100 at final concentrations of 1 mg/ml and 0.1%, respectively, and incubating the solution at 37°C for one hour. The solution was ultrasonicated and then centrifuged at 15,000 g for 10 minutes. The supernatant was recovered (200 ml) and protamine sulfate was added to a final concentration of 0.1% to precipitate nucleic acids. The precipitate was discarded through centrifugation in the same fashion, and the resulting solution was used as a crude enzyme extract.

The activity of the crude enzyme extract was determined toward various synthetic peptides as shown in Table 8. The results demonstrated that the crude enzyme extract possessed dipeptidyl peptidase IV, leucine aminopeptidase, glycine aminopeptidase, and prolyl oligopeptidase activity.

Table 8. Activities of various peptidase activities in the crude enzyme extract solution

	Peptidase	Substrate	Activity (%)
	prolyl oligopeptidase	Z-Ala-Ala-Pro-pNA	46.0
	prolyl oligopeptidase	Z-Gly-Pro-NA	68.7
	dipeptidyl peptidase IV	Gly-Pro-pNA	21.9
5	glycine aminopeptidase	Gly-pNA	100
	leucine aminopeptidase	Leu-pNA	67.8

The crude enzyme extract was precipitated by adding an equal volume of cold acetone. The enzyme precipitate was dissolved in a small volume of 10 mM phosphate pH 6.0 buffer and insoluble substances were removed by centrifugation. The enzyme was  
 10 lyophilized to produce a crude enzyme powder.

**Example 22: Purification of *Sphingomonas capsulata* aminopeptidase I from crude enzyme powder**

The crude enzyme powder described in Example 21 was dissolved in 20 mM  
 15 phosphate pH 7.0 buffer and diluted until the conductivity of the sample was equivalent to the loading buffer, 20 mM phosphate pH 7.0. The sample was loaded onto a Pharmacia Q-Sepharose or Mono Q column pre-equilibrated with 20 mM phosphate pH 7.0 buffer. The flow-throughs from these columns were assayed for aminopeptidase activity with alanine-para-nitroanilide (Ala-pNA) using the procedure described below.

20 A stock solution of 100 mg of Ala-pNA per ml in dimethylsulfoxide was diluted with 50 mM sodium phosphate pH 7.5 buffer to a concentration of 2 mg per ml. The reaction of the aminopeptidase with the para-nitroanilide was initiated when a 10-50  $\mu$ l aliquot of the enzyme solution was added to 200  $\mu$ l of the substrate solution in a microtiter plate well. Analysis of initial rates of hydrolysis of the para-nitroanilide was monitored at  
 25 405 nm at room temperature in a THERMOMax Microplate Reader (Molecular Devices Corp., Sunnyvale, CA, USA).

Aminopeptidase activity was present in the flow-through. The flow-through was concentrated using DIAFLO® PM 10 ultrafiltration membrane (Amicon, Inc., USA) and the pH of the concentrated flow-through was then adjusted to pH 6.0 using 70 mM acetate  
 30 buffer pH 4.0 buffer.

The concentrated flow-through was applied to a Pharmacia Mono S 5/5 pre-packed 7 x 50 mm column (Pharmacia Biotech AB, Uppsala, Sweden) pre-equilibrated with 50 mM MES pH 6.0 buffer. Fractions were assayed as above for aminopeptidase activity. The bound aminopeptidase activity was eluted with a gradient from 0 to 0.2 M NaCl in 50 mM MES pH 6.0 buffer. The fractions with significant activity were then concentrated again using a PM 10 ultrafiltration membrane and then equilibrated in 50 mM phosphate pH 7.0 buffer containing 0.5 M  $(\text{NH}_4)_2\text{SO}_4$ .

The concentrated sample was then loaded onto a Phenyl Superose column pre-equilibrated with 50 mM phosphate pH 7.0 buffer containing 0.5 M  $(\text{NH}_4)_2\text{SO}_4$ . The enzyme was eluted with a gradient from 0.5 M ammonium sulfate containing 50 mM phosphate buffer to 50 mM phosphate buffer containing no ammonium sulfate. Active fractions were pooled.

SDS-PAGE analysis of the purified aminopeptidase revealed one band with a molecular weight of 67 kDa. The purified aminopeptidase was designated *Sphingomonas capsulata* aminopeptidase I.

**Example 23: Purification of *Sphingomonas capsulata* aminopeptidase I from crude enzyme powder**

The crude enzyme powder described in Example 21 was dissolved in distilled water and loaded onto a CM Sepharose CL-6B column (Pharmacia Biotech, Uppsala, Sweden) pre-equilibrated with 15 mM sodium phosphate buffer pH 6.0 buffer. Aminopeptidase I activity was eluted with a linear gradient of 15 mM to 60 mM sodium phosphate buffer (pH 6.0). Fractions of 7.4 ml are collected and assayed for aminopeptidase activity as described in Example 22.

Active fractions were pooled and dialyzed against 15 mM phosphate pH 6.0 buffer. The dialysate was sequentially loaded onto a hydroxylapatite column equilibrated with 15 mM sodium phosphate pH 6.0 buffer. Aminopeptidase I activity was eluted with a linear gradient of 15 mM to 300 mM sodium phosphate 6.0 buffer. Fractions were collected and assayed for aminopeptidase activity. Active fractions were pooled, dialyzed against distilled water, and lyophilized.

**Example 24: Purification of *Sphingomonas capsulata* aminopeptidase I**

*Sphingomonas capsulata* aminopeptidase I was purified from a culture broth supernatant produced by cultivation of *Sphingomonas capsulata* strain IFO 12533 for 15 hours at 31°C, 250 rpm, and an initial pH of 7.45 in 1.5 liters of medium composed of per liter 10 g of bactopectone, 5 g of yeast extract, 3 g of NaCl, 2 g of K<sub>2</sub>HPO<sub>4</sub>, 0.1 g of MgSO<sub>4</sub>·7H<sub>2</sub>O, and 5 g of glucose (autoclaved separately).

Aminopeptidase I activity was measured with alanine-para-nitroanilide (Ala-pNA)-as described in Example 22.

The culture broth supernatant (approximately 1 liter) prepared by centrifugation, filtered using a Whatman glass microfiber filter (Whatman, Maidstone, England), filtered using Nalgene Filterware equipped with a 0.22 mm filter, and concentrated using an Amicon Spiral Ultrafiltration System (Amicon, New Bedford, MA, USA), was equilibrated with 10 mM sodium phosphate pH 6.0 buffer until the conductivity and pH were equal to the loading buffer, 50 mM MES pH 6.0. The filtered solution was loaded onto a 24 x 390 mm column containing approximately 180 ml of SP-Sepharose, Fast Flow (Pharmacia Biotech AB, Uppsala, Sweden) pre-equilibrated with 50 mM MES pH 6.0 buffer. Protein with aminopeptidase I activity was eluted with a 240 ml gradient from 0 to 0.2M NaCl in 50 mM MES pH 6.0 buffer. Fractions with aminopeptidase I activity were pooled, desalted using a DIAFLO™ PM 10 ultrafiltration membrane (Amicon, New Bedford, MA, USA), and equilibrated with 20 mM sodium phosphate pH 7.0 buffer.

The pooled solution was then loaded onto a Pharmacia MonoQ Beads column pre-equilibrated with 20 mM sodium phosphate pH 7.0 buffer. Protein with aminopeptidase I activity did not bind to the column and was collected in the flow-through. The flow-through was concentrated using a PM 10 membrane system as above, and the pH adjusted to 6.0 with 70 mM sodium acetate pH 4.0 buffer.

The concentrated flow-through was loaded onto a Pharmacia Mono S column pre-equilibrated with 50 mM MES pH 6.0 buffer. The aminopeptidase was eluted with a 60 ml gradient from 0 to 0.2 M NaCl in 50 mM MES pH 6.0 buffer. The fractions with significant Ala-pNA activity were then pooled, concentrated, and equilibrated with 50 mM phosphate pH 7.0 buffer containing 0.5 M (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> using a PM 10 membrane system as above.

Finally, the concentrated sample was loaded onto a Pharmacia Phenyl Superose 5/5 pre-packed 7 x 50 mm column (Pharmacia Biotech AB, Uppsala, Sweden) pre-equilibrated with 50 mM phosphate pH 7.0 buffer containing 0.5 M  $(\text{NH}_4)_2\text{SO}_4$ . Protein with aminopeptidase I activity was then eluted with a 30 ml gradient from 0.5 to 0 M  $(\text{NH}_4)_2\text{SO}_4$  in 50 mM phosphate pH 7.0 buffer. Fractions containing aminopeptidase I activity were analyzed by SDS-PAGE and then pooled.

SDS-PAGE analysis of the purified *Sphingomonas capsulata* aminopeptidase I revealed one band with a molecular weight of 67 kDa.

**Example 25: Amino acid sequencing of *Sphingomonas capsulata* aminopeptidase I (67 kDa)**

A 20  $\mu\text{l}$  sample of the purified *Sphingomonas capsulata* aminopeptidase I described in Example 22 was electrophoresed and subsequently blot-transferred to a PVDF membrane using 10 mM CAPS (3-[cyclohexylamino]-1-propanesulfonic acid) pH 11 in 10% methanol for 2 hours. The PVDF membrane was stained with 0.1% Coomassie Blue R-250 in 40% methanol/1% acetic acid for 20 seconds and destained in 50% ethanol to observe the protein bands. The major band of 67 kDa was excised and subjected to amino terminal sequencing on an Applied Biosystems Model 476A Protein Sequencer using a blot cartridge and liquid phase TFA delivery according to the manufacturers instructions. The protein was found to be N-terminally blocked to Edman sequencing chemistry.

A 1.0 ml sample of the purified aminopeptidase I described in Example 22 was dried on a Savant Speed Vac AS160 and then reconstituted with 300  $\mu\text{l}$  of 70% formic acid (aqueous). A few crystals of cyanogen bromide were added and incubated at room temperature in the dark overnight. The sample was redried in the Speed Vac and reconstituted in Tricine sample buffer (Novex, San Diego, CA, USA). The cyanogen bromide cleavage fragments were separated using a 10-20% Tricine SDS-polyacrylamide gel into bands of 42, 30, 17, 15, 10, 6, and 4 kDa and blot-transferred to a PVDF membrane. The 6, 10, 15, 17, 30, and 42 kDa bands were excised and subjected to amino terminal sequencing. The N-terminal sequence of the 10 kDa band was determined to contain the following sequence while the N-terminal sequences of the other bands were inconclusive: AVNGDAYDADKLKGAITNAKTGNPGAGRPI (SEQ ID NO. 11).

**Example 26: Characterization of *Sphingomonas capsulata* aminopeptidase I (67 kDa)**

Stock solutions of 100 mg of each para-nitroanilide per ml of dimethylsulfoxide were diluted with 50 mM sodium phosphate pH 7.5 buffer to concentrations of 2 mg per ml. Where the substrates were incompletely soluble, their suspensions were used (shown with an asterisk in Table 9 below). The reaction of the *Sphingomonas capsulata* aminopeptidase I with each para-nitroanilide was initiated when a 10  $\mu$ l aliquot of the enzyme solution in 50 mM sodium phosphate pH 7.0 was added to 190  $\mu$ l of a substrate solution in a 96 well microtiter plate. Analysis of initial rates of hydrolysis of the para-nitroanilides was monitored at 405 nm and 25°C in a THERMOMax Microplate Reader (Molecular Devices Corp., Sunnyvale, CA, USA). The results (Table 9) showed that the aminopeptidase I preferably hydrolyzed Ala-pNA, but also hydrolyzed Gly-pNA. However, among the dipeptide substrates the aminopeptidase I hydrolysed Gly-Phe-pNA more quickly than Ala-Ala-pNA.

Table 9. Substrate specificity of *Sphingomonas capsulata* aminopeptidase I

Amino acid p-nitroanilides	Relative activity (%)
Ala	100
Met	24
Gly*	20
Leu	18.5
Glu*	6
Asp	4.5
Lys	6
Ile	0.5
Val	0.5
Phe*	0
Pro	0

The pH optimum for the 67 kDa aminopeptidase was determined using the following protocol. The buffer solutions at different pH's were prepared by adding distilled water to 4.25 g of sodium acetate and 3.78 g of Tris (free base) to a final volume of 250 ml and adjusting the pH to 8.5, 8.0, 7.5, 7.0, 6.5, 5.80, 5.5, and 5.0 with 36.5-38% HCl. Aliquots of 10 ml were removed at each pH. A 20  $\mu$ l volume of a 100 mg/ml solution of

Ala-pNA in DMSO was added to 980  $\mu$ l of each buffer solution. The pH was then determined to be 8.5, 8.0, 7.57, 7.30, 7.09, 6.68, 6.14, and 5.25 for the buffer solutions after the addition of the substrate. Another solution of substrate at a concentration of 2 mg/ml was prepared at the various pH's. The reaction was initiated by the addition of 10  $\mu$ l of enzyme solution, diluted 5-fold in 10 mM Tris-HCl pH 7.5, to 200  $\mu$ l of substrate at the various pHs at room temperature and monitored at 405 nm.

The results shown in Table 10 demonstrated that aminopeptidase I has a pH optimum in the range of 5.3 to 8.5, and more preferably in the range of 7.0 to 7.5 (see Figure 6). There was no detectable autohydrolysis of Ala-pNA in the pH range 5.25-8.5. At pH 5.5, hydrolysis of Ala-pNA catalyzed by aminopeptidase I did not follow Michaelis-Menten kinetics where the apparent  $K_m$  and  $V_{max}$  had negative values due to the activation of the enzyme by a substrate. At pH 7.5, the  $K_m$  was 2.5 mM.

Table 10. pH profile of *Sphingomonas capsulata* aminopeptidase I

	pH	Relative Activity (%)
15	5.25	24.9
	6.14	56.4
	6.68	78.4
	7.09	99.4
	7.30	100
20	7.57	92.8
	8.0	61
	8.49	24.2

The temperature optimum was determined using Ala-pNA as substrate in 50 mM sodium phosphate pH 7.5 buffer over the temperature range of 30°C to 55°C. The results showed that aminopeptidase I has a temperature optimum in the range of 35°C to 46°C, and more preferably in the range of 40°C to 45°C at pH 7.5 (see Figure 7).

The temperature stability of aminopeptidase I was determined by incubating the enzyme for 20 minutes in 50 mM sodium phosphate pH 7.5 buffer at temperatures in the range of 35°C to 55°C followed by cooling on ice and measuring the residual activity using Ala-pNA as substrate at pH 7.5 as described above. The results showed (see Figure 8) that the aminopeptidase was approximately 100% stable up to 40°C at pH 7.5. At 45°C, the

enzyme retained approximately 60% residual activity, while at 50°C the enzyme was completely inactivated.

**Example 27: Comparison between DH increasing effect of crude and purified**  
***Sphingomonas capsulata* aminopeptidase I**

The DH increasing effect of *Sphingomonas capsulata* aminopeptidase I (67 kDa) was evaluated in soy protein hydrolysis and compared to the performance of the crude enzyme powder prepared as described in Example 21.

The degree of hydrolysis (DH) of the soy protein was determined as follows. The DH, defined as described in by Adler-Nissen (1986, *Enzymic Hydrolysis of Food Proteins*, Elsevier Applied Science Publishers), was determined by reaction of the supernatant with OPA (ortho-phthaldialdehyde, Sigma Chemical Co., St. Louis, MO) essentially as described by Church *et al.*, 1983, *Journal of Dairy Science* 66: 1219-1227 with correction factors as determined by Adler-Nissen, 1979, *Agricultural and Food Chemistry* 27: 1256-1262.

The aminopeptidase I was added in increasing dosage to either a low background (1.5% of the substrate protein) or a high background (6% of the substrate protein) of FLAVOURZYME 1000L™ and a dosage of ALCALASE 2.4L® of 1.5% of the substrate protein. The experiments were carried out as described below:

Hydrolysis was carried out on a 10 ml scale at 50°C for 18 hours. The initial pH was 7 with no pH readjustment during hydrolysis. Inactivation of the enzyme was carried out at 85°C for 3 minutes in a water bath. The substrate concentration was 2% protein from soy bean meal. The substrate was heat treated in a water bath at 85°C for 3 minutes. The enzymes used were FLAVOURZYME 1000L™, ALCALASE 2.4L®, crude enzyme powder (see Example 21), and the purified *Sphingomonas capsulata* aminopeptidase I described in Example 24.

The aminopeptidase dosages used were based on alanyl-aminopeptidase units (AAU) determined by the hydrolysis of Ala-pNa at pH 7.5. One AAU unit of the aminopeptidase I is defined as the quantity of an enzyme which hydrolyses 1.0 micromole of Ala-pNa per minute in a 9.1 mM solution of Ala-pNa at pH 7.5, 22°C, and ionic strength 50 mM.

The specific activity of the purified aminopeptidase I was approximately 12 AAU/mg enzyme. Therefore, a dosage of 0.24 AAU per 200 mg soy protein, for example, corresponded to 0.1 g enzyme per kg soy protein.

The DH as function of dosage of AAU is shown in Figure 9 for low background dosages of FLAVOURZYME™ and in Figure 10 for a high background dosage of FLAVOURZYME™.

Figures 9 and 10 show that the hydrolysates were close to being saturated with AAU at the highest dosages of AAU. The crude enzyme was capable of increasing DH from 44% to 72% when added to a low dosage of FLAVOURZYME™. The purified aminopeptidase I increased DH to 61-62%. Thus, the purified aminopeptidase I was responsible for  $(62-44)/(72-44) \times 100\% = 64\%$  of the DH increasing effect of the crude enzyme. The crude enzyme increased DH from 61% to 77% when added to a high dosage of FLAVOURZYME™. The purified aminopeptidase I increased DH to 71%. Thus, the purified aminopeptidase I was responsible for  $(71-61)/(77-61) \times 100\% = 63\%$  of the increasing effect of the crude enzyme.

An alternative to addition of aminopeptidase I is the addition of more FLAVOURZYME™. The addition of 0.5% extra FLAVOURZYME™ to the background dosage of 1.5% increased DH from 44% to 48%. The effect of adding aminopeptidase I was calculated to be  $(62-48)/(72-48) \times 100\% = 58\%$  of the effect of the crude enzyme.

Likewise, addition of 1% extra FLAVOURZYME™ to the background dosage of 6% FLAVOURZYME™ increased DH from 61% to 63%. The effect of the aminopeptidase I was calculated to be  $(71-63)/(77-63) \times 100\% = 57\%$  of the effect of the crude enzyme.

The highest DH obtained was 77%. Since the DH value was based on total protein and not on soluble protein, the protein solubility was around 85%. Therefore, DH in the soluble protein was around 91%, which was very close to 100%.

#### Example 28: Free amino acid analysis

The % relative increase in the individual free amino acids (FAA) due to AAU additions are shown in Table 11. Hyp, methioninsulphonic acid, and Trp were not included in the Table due to very fluctuating and uncertain results.

Table 11. % Relative increase in FAA due to addition of aminopeptidases

	FAA	1.5% FLAVOURZYME™		6.0% FLAVOURZYME™		1.5% FLAVOURZYME™
		+crude	+67 kDa AP	+crude	+ 67kDa AP	+ 67 kDa AP versus 6.0% FLAVOURZYME™
5	Asp	250.3	164.5	74.8	24.8	24.2
	Glu	195.6	145.9	70.7	31.3	28.7
	Asn	80.5	32.3	36.9	7.6	-15.2
	Ser	149.5	69.3	78.7	41.7	12.5
	Gln	198.6	138.9	51.6	28.1	9.9
10	Gly	353.6	305.7	117.4	92.9	90.6
	His	64.0	30.3	18.8	7.5	-6.8
	Arg	59.6	37.4	18.1	-31.4	-2.9
	Thr	84.3	34.7	21.2	2.4	-18.3
	Ala	200.2	130.3	71.2	36.5	27.3
15	Pro	73.2	32.4	-9.0	-11.5	-39.7
	Tyr	75.4	47.6	13.8	8.5	-6.9
	Val	114.1	44.0	32.5	6.3	-17.7
	Met	47.9	-20.0	42.5	21.1	-46.7
	Cys	5.0	12.6	17.5	9.5	6.3
20	Ile	133.6	48.7	34.0	7.2	-21.0
	Leu	67.4	35.2	16.4	5.2	-9.1
	Phe	62.6	41.8	13.3	7.2	-4.5
	Lys	105.5	62.4	28.2	13.8	-1.4
	total	110.1	64.5	36.9	10.3	0.0
25	DH	59.6	34.8	24.4	14.2	-2.2

The results showed that when the crude or purified *Sphingomonas capsulata* aminopeptidase I was added, Gly was the amino acid which showed the highest increase. Other amino acids, which showed increased release were Ala, Glu, Gln, Asp and Ser, but for these amino acids the crude enzyme appeared to release more than the purified aminopeptidase I alone probably due to the presence of other aminopeptidases in the crude enzyme.

A high DH hydrolysate was produced by use of a high dosage of FLAVOURZYME™. The same high DH and release of FAA were obtained by using a low dosage of FLAVOURZYME™ supplemented with 67 kDa aminopeptidase I or the crude enzyme. According to Table 12, a hydrolysate obtained by use of a low dosage of  
5 FLAVOURZYME™ supplemented with 67 kDa aminopeptidase I will have a higher level of especially Gly, but also Ala, Glu and Asp and a lower level of Met, Pro and Ile as compared with hydrolysates obtained by using a high dosage of FLAVOURZYME™ alone.

10 **Example 29: DH increasing effect of *Sphingomonas capsulata* aminopeptidase I in gelatin hydrolysis**

The DH increasing effect of the *Sphingomonas capsulata* aminopeptidase I was tested in gelatin hydrolysis.

The aminopeptidase I was added in increased dosage to either a low or a high background of FLAVOURZYME™ and ALCALASE® as performed in Example 27.

15 Hydrolysis was carried out in 200 µl reactions in Eppendorf tubes. The substrate gelatin (Merck) was dissolved in distilled water at 85°C for 5 minutes. After cooling to 50°C, the pH was adjusted to 6.5. The final gelatin concentration was adjusted to 2% after the addition of enzymes. The substrate concentration in each reaction was calculated to be 4 mg.

20 The enzymes used were FLAVOURZYME™, ALCALASE®, crude enzyme powder, purified aminopeptidase I. Glycine aminopeptidase unit (GAPU) of both crude and purified enzyme was measured in 50 mM Tris-HCl pH 7.5 buffer at 37°C using Gly-pNA as a substrate. Aminopeptidase I was assayed at 37°C in 50 mM Tris-HCl (pH 7.5). Gly-pNA (Bachem Feinchemikalien AG, Bubendorf, Switzerland) was dissolved in 40%  
25 dioxane at a concentration of 2.5 mg/ml and 1.5 volume of 50 mM Tris-HCl (pH 7.5) was added to a substrate concentration of 1 mg/ml. The enzyme sample was diluted in 500 µl of the same buffer and 100 µl of the substrate solution was added and incubated at 37°C for 5 minutes. The reaction was terminated by the addition of 300 µl of 1 M sodium acetate pH 4.0 buffer. For the blank reaction, the stop solution was added to the enzyme solution  
30 and incubated for 5 minutes at 37°C, and then the substrate solution was added. The absorbance at 410 nm was measured for both the sample and blank reactions. The enzyme

activity was calculated using the molecular extinction coefficient at 410 nm for pNA as 9480  $M^{-1} cm^{-1}$ . One unit of GAPU was defined as the quantity of enzyme that hydrolyses 1 micromole of Gly-pNA at 37°C per minute under the conditions described above. The specific activities of the crude and purified aminopeptidase I used were 0.725 GAPU/mg and 6.45 GAPU/mg, respectively. The enzymes were dosed to the 4 mg protein according to the scheme in Table 12.

Table 12

Tube no.	FLAVOURZYME™ (μg)	ALCALASE® (μg)	Aminopeptidase I (μg)
1	80 (2%)	40 (1%)	
2	"	"	
3	"	"	
4	"	"	
5	"	"	8 (0.2%) ≈ 0.05 U
6	"	"	31 (0.77%) ≈ 0.2 U
7	"	"	78 (2%) ≈ 0.5 U
8	"	"	155 (4%) ≈ 1.0 U
9	280 (7%)	40 (1%)	
10	"	"	
11	"	"	
12	"	"	
13	"	"	8 (0.2%) ≈ 0.05 U
14	"	"	31 (0.77%) ≈ 0.2 U
15	"	"	78 (2%) ≈ 0.5 U
16	"	"	155 (4%) ≈ 1.0 U

Enzyme/substrate ratios are given in parentheses after amounts of enzymes shown as weight.

The hydrolysis reactions were performed at 50°C for 18 hours. Enzymes were inactivated at 85°C for 5 minutes followed by centrifugation. DH was calculated on the basis of the total protein content of hydrolysate using the OPA method.

The DH-increasing effect of purified aminopeptidase I shown in Figures 11 and 12 demonstrated that addition of the crude and the purified enzyme (0.2 U/4 mg gelatin) to the

low FLAVOURZYME™ background increased DH from 38% to 67% and 61%, respectively. The DH increasing effect was almost saturated at this dose.

When the dose of FLAVOURZYME™ was increased up to 7%, the control DH increased to 43%. However, the DH obtained with purified aminopeptidase I was 61% which almost coincided with those obtained in the low FLAVOURZYME™ background.

These results indicated that the *Sphingomonas capsulata* aminopeptidase I hydrolyses proteins to an extremely high DH. Furthermore, using aminopeptidase I, the dosage of other proteolytic enzymes can be reduced to obtain the same DH.

10

#### Deposit of Biological Materials

The following biological material has been deposited under the terms of the Budapest Treaty with the Agricultural Research Service Patent Culture Collection, Northern Regional Research Center, 1815 University Street, Peoria, Illinois, 61604, and given the following accession number:

15

Deposit	Accession Number	Date of Deposit
E. coli DH5α pEJG18	NRRL B-21677	April 4, 1997

## SEQUENCE LISTING

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## (i) APPLICANT:

(A) NAME: Novo Nordisk A/S  
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## (i) APPLICANT:

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(C) CITY: Fuji City, Shizuoka, Tokyo 416  
(D) COUNTRY: Japan  
(E) POSTAL CODE: (ZIP):  
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(ii) TITLE OF THE INVENTION: Methods for Producing Protein Hydrolysates

(iii) NUMBER OF SEQUENCES: 11

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## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US98/09998  
(B) FILING DATE: 15-MAY-1998  
(C) CLASSIFICATION:

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(A) TELEPHONE: 212-867-0123  
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(C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGGTCGC	TTTTGTGGGC	TTCGTTGCTT	TCGGGCGTGT	TGGCTGGGAG	GGCGCTTGTT	60
TCGCCGGATG	AGTTCCCCGA	GGATATTCAG	TTGGAAGATC	TGCTGGAAGG	ATCCCAACAG	120
CTTGAGGACT	TCGCCTATGC	CTACCCCGAG	CGCAATCGCG	TCTTTGGTGG	TAAAGCCCAC	180
GACGACACGG	TTAACTATCT	CTACGAGGAG	CTGAAGAAGA	CTGGCTACTA	TGATGTCTAC	240
AAGCAGCCTC	AGGTGCACCT	GTGGAGCAAT	GCCGACCAGA	CGCTCAAGGT	GGGCGATGAG	300
GAAATCGAGG	CGAAGACCAT	GACCTACAGT	CCCAGCGTCG	AGGTCAACCG	CGATGTAGCC	360
GTCGTCAAGA	ACCTGGGATG	CAGCGAGGCG	GATTACCCAT	CCGATGTCGA	GGGCAAGGTC	420
GCCCTGATCA	AGCGTGGAGA	ATGCCCCGTT	GGCGACAAGT	CGGTTCTCGC	TGCCAAAGCC	480
AAGGCCGCGG	CTTCGATTGT	CTATAACAAT	GTGGCCGGAT	CCATGGCGGG	CACCCTTGGC	540
GCGGCGCAGA	GTGATAAGGG	ACCGTATTCG	GCCATTGTCG	GTATCAGCTT	GGAGGATGGC	600
CAGAAGCTGA	TCAAGCTTGC	TGAGGCTGGA	TGCTATCTGT	TGGATCTGTG	GGTGGATAGT	660
AAGCAGGAGA	ACCGTACGAC	GTATAACGTT	GTCGCGCAGA	CGAAGGGCGG	CGATCCGAAC	720
AACGTCGTCG	CGCTGGGTGG	CCACACGGAC	TCAGTCGAGG	CGGGCCCTGG	TATCAACGAC	780
GATGGCTCGG	GCATTATTAG	CAACTTGGTC	ATTGCCAAAG	CGCTCACGCA	GTA CTCCGTC	840
AAGAATGCCG	TGCGCTTCCT	CTTCTGGACA	GCAGAGGAGT	TGCGTCTGCT	GGGCAGCAAC	900
TACTACGTCT	CCCATCTGAA	TGCCACCGAG	CTGAACAAGA	TCCGACTGTA	CCTGAACTTC	960
GACATGATCG	CCTCACCTAA	CTACGCCCTC	ATGATCTATG	ACGGTGATGG	ATCGGCGTTC	1020
AACCAGAGCG	GACCGGCCCG	TTCCGCCCCAG	ATCGAGAAAC	TGTTGAGGGA	CTACTACGAC	1080
TCCATCGACC	TGCCTCATAT	CCCCACCCAG	TTTGACGGAC	GTTCCGACTA	CGAGGCCCTT	1140
ATCCTGAACG	GCATTCCGTC	CGGTGGACTC	TTCACGGGCG	CCGAGGGCAT	CATGTCCGAA	1200
GAGAACGCAA	GCCGCTGGGG	AGGTCAAGCC	GGCGTGCCCT	ACGACGCCAA	CTACCACGCC	1260
GCGGGAGACA	ACATGACCAA	CCTCAACCAT	GAAGCCTTCC	TGATCAACTC	CAAAGCCACC	1320
GCCTTCGCCG	TCGCCACCTA	CGCCAACGAC	CTCTCCTCGA	TCCCCAAACG	GAATACCACA	1380
TCCTCCTTGC	ACCGACGAGC	CCGCACCATG	CGACCATTCT	GCAAGAGAGC	TCCGAAGACA	1440
CACGCTCAGC	TATCAGGATC	CGGATGCTGG	CATTCTCAAG	TCGAGGCATA	G	1491

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Ser	Leu	Leu	Trp	Ala	Ser	Leu	Leu	Ser	Gly	Val	Leu	Ala	Gly
1				5					10					15	
Arg	Ala	Leu	Val	Ser	Pro	Asp	Glu	Phe	Pro	Glu	Asp	Ile	Gln	Leu	Glu
			20					25					30		
Asp	Leu	Leu	Glu	Gly	Ser	Gln	Gln	Leu	Glu	Asp	Phe	Ala	Tyr	Ala	Tyr
		35				40					45				
Pro	Glu	Arg	Asn	Arg	Val	Phe	Gly	Gly	Lys	Ala	His	Asp	Asp	Thr	Val
		50			55						60				
Asn	Tyr	Leu	Tyr	Glu	Glu	Leu	Lys	Lys	Thr	Gly	Tyr	Tyr	Asp	Val	Tyr
65				70					75					80	
Lys	Gln	Pro	Gln	Val	His	Leu	Trp	Ser	Asn	Ala	Asp	Gln	Thr	Leu	Lys
			85					90						95	
Val	Gly	Asp	Glu	Glu	Ile	Glu	Ala	Lys	Thr	Met	Thr	Tyr	Ser	Pro	Ser
			100					105					110		
Val	Glu	Val	Thr	Ala	Asp	Val	Ala	Val	Val	Lys	Asn	Leu	Gly	Cys	Ser
		115				120					125				
Glu	Ala	Asp	Tyr	Pro	Ser	Asp	Val	Glu	Gly	Lys	Val	Ala	Leu	Ile	Lys
		130			135						140				
Arg	Gly	Glu	Cys	Pro	Phe	Gly	Asp	Lys	Ser	Val	Leu	Ala	Ala	Lys	Ala
145					150				155					160	
Lys	Ala	Ala	Ala	Ser	Ile	Val	Tyr	Asn	Asn	Val	Ala	Gly	Ser	Met	Ala

Gly	Thr	Leu	Gly	165	Ala	Ala	Gln	Ser	Asp	170	Lys	Gly	Pro	Tyr	Ser	175	Ala	Ile
Val	Gly	Ile	Ser	180	Leu	Glu	Asp	Gly	185	Gln	Lys	Leu	Ile	Lys	190	Leu	Ala	Glu
Ala	Gly	Ser	Val	195	Ser	Val	Asp	200	Leu	Trp	Val	Asp	Ser	205	Lys	Gln	Glu	Asn
Arg	Thr	Thr	Tyr	210	Asn	Val	Val	Ala	215	Gln	Thr	Lys	Gly	220	Gly	Asp	Pro	Asn
Asn	Val	Val	Ala	225	Leu	Gly	Gly	His	230	Thr	Asp	Ser	Val	235	Glu	Ala	Gly	Pro
Gly	Ile	Asn	Asp	245	Asp	Gly	Ser	Gly	250	Ile	Ile	Ser	Asn	255	Leu	Val	Ile	Ala
Lys	Ala	Leu	Thr	260	Gln	Tyr	Ser	Val	265	Lys	Asn	Ala	Val	270	Arg	Phe	Leu	Phe
Trp	Thr	Ala	Glu	275	Glu	Phe	Gly	Leu	280	Leu	Gly	Ser	Asn	285	Tyr	Tyr	Val	Ser
His	Leu	Asn	Ala	290	Thr	Glu	Leu	Asn	295	Lys	Ile	Arg	Leu	300	Tyr	Leu	Asn	Phe
Asp	Met	Ile	Ala	305	Ser	Pro	Asn	Tyr	310	Ala	Leu	Met	Ile	315	Tyr	Asp	Gly	Asp
Gly	Ser	Ala	Phe	325	Asn	Gln	Ser	Gly	330	Pro	Ala	Gly	Ser	335	Ala	Gln	Ile	Glu
Lys	Leu	Phe	Glu	340	Asp	Tyr	Tyr	Asp	345	Ser	Ile	Asp	Leu	350	Pro	His	Ile	Pro
Thr	Gln	Phe	Asp	355	Gly	Arg	Ser	Asp	360	Tyr	Glu	Ala	Phe	365	Ile	Leu	Asn	Gly
Ile	Pro	Ser	Gly	370	Gly	Leu	Phe	Thr	375	Gly	Ala	Glu	Gly	380	Ile	Met	Ser	Glu
Glu	Asn	Ala	Ser	385	Arg	Trp	Gly	Gly	390	Gln	Ala	Gly	Val	395	Ala	Tyr	Asp	Ala
Asn	Tyr	His	Ala	405	Ala	Gly	Asp	Asn	410	Met	Thr	Asn	Leu	415	Asn	His	Glu	Ala
Phe	Leu	Ile	Asn	420	Ser	Lys	Ala	Thr	425	Ala	Phe	Ala	Val	430	Ala	Thr	Tyr	Ala
Asn	Asp	Leu	Ser	435	Ser	Ile	Pro	Lys	440	Arg	Asn	Thr	Thr	445	Ser	Ser	Leu	His
Arg	Arg	Ala	Arg	450	Thr	Met	Arg	Pro	455	Phe	Gly	Lys	Arg	460	Ala	Pro	Lys	Thr
His	Ala	His	Val	465	Ser	Gly	Ser	Gly	470	Cys	Trp	His	Ser	475	Gln	Val	Glu	Ala
				485										490				495

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: None

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Cys	Cys	Ile	Gly	Ala	Tyr	Gly	Ala	Arg	Thr	Thr	Tyr	Cys	Cys	Ile	Gly
1				5					10					15	
Ala	Arg	Gly	Ala												
				20											

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg	Thr	Thr	Tyr	Thr	Ile	Ala	Cys	Ile	Ala	Cys	Ile	Gly	Cys	Ile
1				5				10					15	
Ala	Cys	Arg	Thr	Cys	Ile	Gly	Cys	Ile	Gly	Thr	Ile	Ala	Cys	Tyr
			20				25						30	
Cys	Ile	Ala	Cys											
			35											

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 537 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	His	Phe	Ser	Leu	Lys	Gln	Leu	Ala	Val	Ala	Ala	Phe	Tyr	Ala	Thr
1				5					10					15	
Asn	Leu	Gly	Ser	Ala	Tyr	Val	Ile	Pro	Gln	Phe	Phe	Gln	Glu	Ala	Phe
			20					25					30		
Gln	Gln	Glu	Glu	Pro	Ile	Glu	Asn	Tyr	Leu	Pro	Gln	Leu	Asn	Asp	Asp
		35				40						45			
Asp	Ser	Ser	Ala	Val	Ala	Ala	Asn	Ile	Pro	Lys	Pro	His	Ile	Pro	Tyr
	50					55					60				
Phe	Met	Lys	Pro	His	Val	Glu	Ser	Glu	Lys	Leu	Gln	Asp	Lys	Ile	Lys
65					70				75					80	
Val	Asp	Asp	Leu	Asn	Ala	Thr	Ala	Trp	Asp	Leu	Tyr	Arg	Leu	Ala	Asn
			85					90					95		
Tyr	Ser	Thr	Pro	Asp	Tyr	Gly	His	Pro	Thr	Arg	Val	Ile	Gly	Ser	Lys
			100					105				110			
Gly	His	Asn	Lys	Thr	Met	Glu	Tyr	Ile	Leu	Asn	Val	Phe	Asp	Asp	Met
		115				120						125			
Gln	Asp	Tyr	Tyr	Asp	Val	Ser	Leu	Gln	Glu	Phe	Glu	Ala	Leu	Ser	Gly
	130					135				140					
Lys	Ile	Ile	Ser	Phe	Asn	Leu	Ser	Asp	Ala	Glu	Thr	Gly	Lys	Ser	Phe
145					150					155					160
Ala	Asn	Thr	Thr	Ala	Phe	Ala	Leu	Ser	Pro	Pro	Val	Asp	Gly	Phe	Val
				165				170					175		
Gly	Lys	Leu	Val	Glu	Ile	Pro	Asn	Leu	Gly	Cys	Glu	Glu	Lys	Asp	Tyr
		180				185						190			
Ala	Ser	Val	Val	Pro	Pro	Arg	His	Asn	Glu	Lys	Gln	Ile	Ala	Leu	Ile
	195					200						205			
Glu	Arg	Gly	Lys	Cys	Pro	Phe	Gly	Asp	Lys	Ser	Asn	Leu	Ala	Gly	Lys
	210					215					220				
Phe	Gly	Phe	Thr	Ala	Val	Val	Ile	Tyr	Asp	Asn	Glu	Pro	Lys	Ser	Lys
225					230				235					240	
Glu	Gly	Leu	His	Gly	Thr	Leu	Gly	Glu	Pro	Thr	Lys	His	Thr	Val	Ala
			245					250					255		
Thr	Val	Gly	Val	Pro	Tyr	Lys	Val	Gly	Lys	Lys	Leu	Ile	Ala	Asn	Ile
		260						265				270			
Ala	Leu	Asn	Ile	Asp	Tyr	Ser	Leu	Tyr	Phe	Ala	Met	Asp	Ser	Tyr	Val
	275					280						285			
Glu	Phe	Ile	Lys	Thr	Gln	Asn	Ile	Ile	Ala	Asp	Thr	Lys	His	Gly	Asp
	290					295					300				
Pro	Asp	Asn	Ile	Val	Ala	Leu	Gly	Ala	His	Ser	Asp	Ser	Val	Glu	Glu
	305				310					315				320	
Gly	Pro	Gly	Ile	Asn	Asp	Asp	Gly	Ser	Gly	Thr	Ile	Ser	Leu	Leu	Asn
			325					330					335		
Val	Ala	Lys	Gln	Leu	Thr	His	Phe	Lys	Ile	Asn	Asn	Lys	Val	Arg	Phe
		340						345					350		
Ala	Trp	Trp	Ala	Ala	Glu	Glu	Glu	Gly	Leu	Leu	Gly	Ser	Asn	Phe	Tyr
	355					360					365				
Ala	Tyr	Asn	Leu	Thr	Lys	Glu	Glu	Asn	Ser	Lys	Ile	Arg	Val	Phe	Met

370	375	380
Asp Tyr Asp Met Met	Ala Ser Pro Asn Tyr	Glu Tyr Glu Ile Tyr Asp
385	390	395
Ala Asn Asn Lys Glu	Asn Pro Lys Gly Ser	Glu Glu Leu Lys Asn Leu
405	410	415
Tyr Val Asp Tyr Tyr	Lys Ala His His	Leu Asn Tyr Thr Leu Val Pro
420	425	430
Phe Asp Gly Arg Ser	Asp Tyr Val Gly Phe	Ile Asn Asn Gly Ile Pro
435	440	445
Ala Gly Gly Ile Ala	Thr Gly Ala Glu Lys	Asn Asn Val Asn Asn Gly
450	455	460
Lys Val Leu Asp Arg	Cys Tyr His Gln Leu	Cys Asp Asp Val Ser Asn
465	470	475
Leu Ser Trp Asp Ala	Phe Ile Thr Asn Thr	Lys Leu Ile Ala His Ser
485	490	495
Val Ala Thr Tyr Ala	Asp Ser Phe Glu Gly	Phe Pro Lys Arg Glu Thr
500	505	510
Gln Lys His Lys Glu	Val Asp Ile Leu Asn	Ala Gln Gln Pro Gln Phe
515	520	525
Lys Tyr Arg Ala Asp	Phe Leu Ile Ile	
530	535	

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGATGAGGT CGCTTTTGTG GGC

23

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGATGCATC TATGCCTCGA CTT

23

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATTTAAATCA CCATGAGGTC GCTTTTGTGG GC

32

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTTAATTA ACTATGCCTC GACTTGAGAA TG

32

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1926 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

CAGGTGCAGC CGGCGAGCAA CAGCCGCCCG ATGGCAGTGC CGATCGCTCA TGGGGTGCCC 60
GATGCGCAGG ACGTGCCCTA TCCC GGACAG ATCGGGCTGC AGATCGATGC CACCGATCTG 120
GCCACCGGGG CGTTCCGGGT GGTGGAAACC GTGCCGGTGG CGGCCGATGC CAAGGAACTG 180
ATCCTGCAAC TGCCGGCCTG GCTGCCGGGT GAGCATGGCA ATCGCGGCCC CGTGGCCGAG 240
CTGGCCGGCA TCACGTTTGA AGCCAAGGGT CAGAAGCTGG CCTGGACCCG CGACCCGGTG 300
GAAGTGAACG CGTTCCACAT CCCCCTGCCC GCCGGCACCA GCGAAGTGGT GGCCCCGCTT 360
ATCCACACCT CGCCGCTGCG CGACAGCGAA GGCCGCATCA CCGTTACGCG CGAAATGCTC 420
AACGTGCAGT GGGAGAAGAT GAGCCTCTAT CCCGCCGGTC ACTATGTGCG GCAGATCAAG 480
GTGCGTCCCA CCGTCAGCTT CCGCAGGGG TGGACCGTGT TCACCGCGCT GGATGGCAAG 540
ACGCAGAGCG GCGCGGGCAA TACCGTGA CTGGGCCGAAA CCGACTATGA AACCTGGT 600
GATTCGCCGA TCTTTGCCGG GCTCTATGCC GCGCGGCATG ATCTGGGCCA CAACGTCTAT 660
TTCGATCTGG TGGCCGACAA GCCCGAGCTG CTGGCGATCA AGCCGGAAAA CCTGGCCGCC 720
TATCGCAACC TGGCCGACGA AGCCGTGGGC GCATTGCGCG CGCGCCATTT CGATCACTAC 780
GATTTCTGCT TCGCGCTGAC CGATCGCATG GGCAGCATCG GCCTGGAACA CCACCGTTCC 840
AGCGAAAACC AGCAGGAACC CAAGAGCCTG ACCGACTGGG CCGCCTATGA CTGGGACCGC 900
AACGTGATCG CCCACGAATT CAGCCACAGC TGGGATGGCA AGTATCGCCG CTCGGCCAAG 960
CTGTGGAGCG CCGACTATCG CCAGCCGATG CAGGACAACC TGCTGTGGGT CTATGAAGGG 1020
CAGACGCAGT TCTGGGGCCT GGTCTTGGCC GCACGCTCGG GCGTGCAGAG CAAGGACGTG 1080
GTCTTGGGCA GCCTCGCCAA CTATGCCGGC ACGTTCACCC AGACCGCCGG GCGCGACTGG 1140
CGCTCGGTGG AAGACACGAC GATGGATCCC ATCTTCGCCG CCCGCAAGCC CAAGCCCTAT 1200
TCCTCGCTTA CCCGTAACGA GGACTATTAC ACCGAAGGCG CGCTGGTGTG GCTGGAAGCG 1260
GACCAGATCA TCCGCGATGG CACCGGCGGC AAGAAGGGCC TGGATGATTT CGCCAAGGCG 1320
TTCTTTGGCG TGCGCGACGG CGATTGGGGC GTGCTGACCT ATGAATTCTG TGACGTGGTC 1380
AAGACCCTCA ACGGCGTCTA TCCCTATGAC TGGGCCACGT TCCTCAAGAC CCGCCTGCAG 1440
ACGCCGGGCC AGCCGGTGCC GCTCGGCGGG ATCGAGCGCG GCGGCTACAA GCTGGAATTC 1500
AAGGACGAGC CCAACCCCTA TGACAAGGCG CGCATGGCCG ATGCCAAGGT GCTCAGCCTG 1560
TTCAACTCGC TGGGCGTGAC GCTGGACAAG GACGGCAAAG TCACCGCCTC GCGCTGGGAT 1620
GGCCCGGCGT TCAAGGCGGG GCTGGTTTCG GGCATGCAGG TGATGGCCGT GAACGGCGAC 1680
GCCTATGACG CGGACAAGCT CAAGGGCGCG ATCACCAATG CCAAGACCGG CAACCCCGGC 1740
GCCGGCCGCC CGATCGAACT GCTGGTCAAG CGTGACGATC GCTTTGTAC GCTGCCGATC 1800
ACCTATGCCG ATGGCCTGCG CTGGCCGTGG CTGGTGCGCA CGGCGCCGGG CACGGCACCG 1860
ACCGGGCTGG ACAAGCTGCT GGCCCCGCAC GCCAGCAAGC TGCCCGTGGG CAAGGCTGCC 1920
AAGTGA

```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Met Arg Lys Thr Pro Gln Gly Ile Gly Leu Leu Ser Ala Leu Ser Thr
 1           5           10           15
Ser Thr Leu Ala Leu Ala Thr Leu Ile Leu Ala Gln Pro Ala Leu Ala
 20           25           30
Gln Val Gln Pro Ala Ser Asn Ser Arg Pro Met Ala Val Pro Ile Ala
 35           40           45
His Gly Val Pro Asp Ala Gln Asp Val Pro Tyr Pro Gly Thr Ile Gly
 50           55           60

```

Leu	Gln	Ile	Asp	Ala	Thr	Asp	Leu	Ala	Thr	Gly	Ala	Phe	Arg	Val	Val
65					70					75					80
Glu	Thr	Val	Pro	Val	Ala	Ala	Asp	Ala	Lys	Glu	Leu	Ile	Leu	Gln	Leu
				85					90					95	
Pro	Ala	Trp	Leu	Pro	Gly	Glu	His	Gly	Asn	Arg	Gly	Pro	Val	Ala	Glu
			100					105					110		
Leu	Ala	Gly	Ile	Thr	Phe	Glu	Ala	Lys	Gly	Gln	Lys	Leu	Ala	Trp	Thr
		115					120					125			
Arg	Asp	Pro	Val	Glu	Val	Asn	Ala	Phe	His	Ile	Pro	Leu	Pro	Ala	Gly
	130					135					140				
Thr	Ser	Glu	Val	Val	Ala	Arg	Phe	Ile	His	Thr	Ser	Pro	Leu	Arg	Asp
145					150					155					160
Ser	Glu	Gly	Arg	Ile	Thr	Val	Thr	Arg	Glu	Met	Leu	Asn	Val	Gln	Trp
			165						170					175	
Glu	Lys	Met	Ser	Leu	Tyr	Pro	Ala	Gly	His	Tyr	Val	Arg	Gln	Ile	Lys
			180					185					190		
Val	Arg	Pro	Thr	Val	Ser	Phe	Pro	Gln	Gly	Trp	Thr	Val	Phe	Thr	Ala
		195					200					205			
Leu	Asp	Gly	Lys	Thr	Gln	Ser	Gly	Ala	Gly	Asn	Thr	Val	Thr	Trp	Ala
	210					215					220				
Glu	Thr	Asp	Tyr	Glu	Thr	Leu	Val	Asp	Ser	Pro	Ile	Phe	Ala	Gly	Leu
225					230					235					240
Tyr	Ala	Ala	Arg	His	Asp	Leu	Gly	His	Asn	Val	Tyr	Phe	Asp	Leu	Val
			245						250					255	
Ala	Asp	Lys	Pro	Glu	Leu	Leu	Ala	Ile	Lys	Pro	Glu	Asn	Leu	Ala	Ala
			260					265					270		
Tyr	Arg	Asn	Leu	Ala	Asp	Glu	Ala	Val	Gly	Ala	Phe	Gly	Ala	Arg	His
	275					280						285			
Phe	Asp	His	Tyr	Asp	Phe	Leu	Leu	Ala	Leu	Thr	Asp	Arg	Met	Gly	Ser
	290					295					300				
Ile	Gly	Leu	Glu	His	His	Arg	Ser	Ser	Glu	Asn	Gln	Gln	Glu	Pro	Lys
305					310					315					320
Ser	Leu	Thr	Asp	Trp	Ala	Ala	Tyr	Asp	Trp	Asp	Arg	Asn	Val	Ile	Ala
			325						330					335	
His	Glu	Phe	Ser	His	Ser	Trp	Asp	Gly	Lys	Tyr	Arg	Arg	Ser	Ala	Lys
			340					345					350		
Leu	Trp	Thr	Pro	Asp	Tyr	Arg	Gln	Pro	Met	Gln	Asp	Asn	Leu	Leu	Trp
	355						360					365			
Val	Tyr	Glu	Gly	Gln	Thr	Gln	Phe	Trp	Gly	Leu	Val	Leu	Ala	Ala	Arg
	370					375					380				
Ser	Gly	Val	Gln	Ser	Lys	Asp	Val	Val	Leu	Gly	Ser	Leu	Ala	Asn	Tyr
385					390					395					400
Ala	Gly	Thr	Phe	Thr	Gln	Thr	Ala	Gly	Arg	Asp	Trp	Arg	Ser	Val	Glu
			405						410					415	
Asp	Thr	Thr	Met	Asp	Pro	Ile	Phe	Ala	Ala	Arg	Lys	Pro	Lys	Pro	Tyr
			420					425					430		
Ser	Ser	Leu	Thr	Arg	Asn	Glu	Asp	Tyr	Tyr	Thr	Glu	Gly	Ala	Leu	Val
	435					440						445			
Trp	Leu	Glu	Ala	Asp	Gln	Ile	Arg	Asp	Gly	Thr	Gly	Gly	Lys	Lys	
	450				455					460					
Gly	Leu	Asp	Asp	Phe	Ala	Lys	Ala	Phe	Phe	Gly	Val	Arg	Asp	Gly	Asp
465					470					475					480
Trp	Gly	Val	Leu	Thr	Glu	Phe	Asp	Asp	Val	Val	Lys	Thr	Leu	Asn	
			485					490					495		
Gly	Val	Tyr	Pro	Tyr	Asp	Trp	Ala	Thr	Phe	Leu	Lys	Thr	Arg	Leu	Gln
			500					505					510		
Thr	Pro	Gly	Gln	Pro	Val	Pro	Leu	Gly	Gly	Ile	Glu	Arg	Gly	Gly	Tyr
	515						520					525			
Lys	Leu	Glu	Phe	Lys	Asp	Glu	Pro	Asn	Pro	Tyr	Asp	Lys	Ala	Arg	Met
	530					535					540				
Ala	Asp	Ala	Lys	Val	Leu	Ser	Leu	Phe	Asn	Ser	Leu	Gly	Val	Thr	Leu
545					550					555					560
Asp	Lys	Asp	Gly	Lys	Val	Thr	Ala	Ser	Arg	Trp	Asp	Gly	Pro	Ala	Phe
			565					570					575		
Lys	Ala	Gly	Leu	Val	Ser	Gly	Met	Gln	Val	Met	Ala	Val	Asn	Gly	Asp
			580				585						590		
Ala	Tyr	Asp	Ala	Asp	Lys	Leu	Lys	Gly	Ala	Ile	Thr	Asn	Ala	Lys	Thr
	595					600						605			
Gly	Asn	Pro	Gly	Ala	Gly	Arg	Pro	Ile	Glu	Leu	Leu	Val	Lys	Arg	Asp

[illegible]

## Claims

### What is claimed is:

- 5 1. A method of producing a protein hydrolysate, comprising adding to a proteinaceous material one or more polypeptide(s) having glycine releasing activity and one or more additional proteases wherein the amount of glycine produced is greater than the amount of glycine produced by the one or more additional proteases alone under the same conditions.
- 10 2. The method of claim 1, wherein the percent increase of glycine is between 25-400%, preferably 50-350%, more preferably 100-350%, even more preferably 150-350%, and most preferably 200-350%.
3. The method of claim 1 or 2, wherein the degree of hydrolysis is between 35-90%,  
15 preferably 45-80%, more preferably 50-75%, even more preferably 55-75%, and most preferably 60-70%.
4. The method of any of claims 1-3, wherein the polypeptide is selected from the group consisting of:  
20 (a) a polypeptide having an amino acid sequence which has at least 50% identity with the amino acid sequence of SEQ ID NO:2;  
(b) a polypeptide encoded by a nucleic acid sequence which hybridizes under medium stringency conditions with (i) the nucleic acid sequence of SEQ ID NO:1, (ii) its complementary strand, or (iii) a subsequence thereof;  
25 (c) an allelic variant of (a) or (b); and  
(d) a fragment of (a), (b), or (c), wherein the fragment has aminopeptidase activity;  
and  
(e) a polypeptide having aminopeptidase activity with physicochemical properties of  
(i) a pH optimum in the range of from about pH 7.27 to about pH 10.95 determined at  
30 ambient temperature in the presence of Ala-para-nitroanilide; (ii) a temperature stability of 90% or more, relative to initial activity, at pH 7.5 determined after incubation for 20 minutes at 60°C in the absence of substrate; and (iii) an activity towards

Xaa-para-nitroanilide wherein Xaa is selected from the group consisting of Leu, Glu, Gly, Ala, and Pro.

5        5.        The method of claim 4, wherein the polypeptide has an amino acid sequence which has a degree of identity to the amino acid sequence of SEQ ID NO:2 of at least about 50%, preferably at least about 60%, preferably at least about 70%, more preferably at least about 80%, even more preferably at least about 90%, most preferably at least about 95%, and even most preferably at least about 97%, which have aminopeptidase activity (hereinafter "homologous polypeptides").

10

6.        The method of claim 4, wherein the polypeptide is obtained from an *Aspergillus oryzae* strain, and most preferably from *Aspergillus oryzae* ATCC 20386 or a mutant strain thereof, *e.g.*, the polypeptide with the amino acid sequence of SEQ ID NO:2.

15

7.        The method of any of claims 1-3, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide having an amino acid sequence which has at least 50% identity with the amino acid sequence of SEQ ID NO:11;

20

(b) a polypeptide encoded by a nucleic acid sequence which hybridizes under medium stringency conditions with (i) the nucleic acid sequence of SEQ ID NO:10, (ii) its complementary strand, or (iii) a subsequence thereof;

(c) an allelic variant of (a) or (b); and

(d) a fragment of (a), (b), or (c), wherein the fragment has aminopeptidase activity; and

25

(e) a polypeptide which (a) has aminopeptidase activity in the pH range between pH 5.0-8.5 measured at 37°C, (b) an isoelectric point (pI) in the range of 7.4-8.5; (c) has aminopeptidase activity in the temperature range of 20-55°C, measured at pH 7.5 using Gly-pNA in Tris-HCl buffer; (d) hydrolyzes Ala-pNA, Gly-pNA, Leu-pNA, Glu-pNA, Asp-pNA, Lys-pNA, Ile-pNA and Val-pNA; (e) does not hydrolyze Phe-pNA nor Pro-pNA; (f) is not  
30        inhibited by phenylmethanesulfonyl fluoride, slightly inhibited by EDTA, di-isopropyl fluoro phosphate, p-chloromercuribenzoic acid and iodoacetic acid, completely inhibited by o-

phenanthrolin, and/or (g) is obtained from a strain belonging to *Sphingomonas* and has a molecular mass of  $67 \pm 5$  kDa.

8. The method of claim 7, wherein the polypeptide has an amino acid sequence which has a degree of identity to the amino acid sequence of SEQ ID NO:11 of at least about 50%, preferably at least about 60%, preferably at least about 70%, more preferably at least about 80%, even more preferably at least about 90%, most preferably at least about 95%, and even most preferably at least about 97%, which have aminopeptidase activity (hereinafter "homologous polypeptides").

9. The method of claim 7, wherein the polypeptide is obtained from a *Sphingomonas capsulata* strain, e.g., *Sphingomonas capsulata* is IFO 12533, which is a bacterial strain kept at the Institute for Fermentation, Osaka, Japan, e.g., the polypeptide with the amino acid sequence of SEQ ID NO:11 (the predicted signal peptide consists of the first 32 amino acids).

10. The method of claim 4, 5, 7, or 8, wherein the polypeptide is obtained from a bacterial source such as a gram positive bacterium, e.g., a *Bacillus* strain, e.g., *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus stearothermophilus*, *Bacillus subtilis*, or *Bacillus thuringiensis*; or a *Streptomyces* strain, e.g., *Streptomyces lividans* or *Streptomyces murinus*; or from a gram negative bacterium, e.g., *E. coli* or *Pseudomonas* sp.

11. The method of claim 4, 5, 7, or 8, wherein the polypeptide is obtained from a fungal source, preferably from a yeast strain such as a *Candida*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomyces*, or *Yarrowia* strain; or a filamentous fungal strain such as an *Acremonium*, *Aspergillus*, *Aureobasidium*, *Cryptococcus*, *Filibasidium*, *Fusarium*, *Humicola*, *Magnaporthe*, *Mucor*, *Myceliophthora*, *Neocallimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Piromyces*, *Schizophyllum*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Tolytocladium*, or *Trichoderma* strain.

12. The method of claim 4, 5, 7, or 8, wherein the polypeptide is obtained from a *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis* or  
5 *Saccharomyces oviformis* strain.

13. The method of claim 4, 5, 7, or 8, wherein the polypeptide is obtained from a *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*,  
10 *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecioides*, *Fusarium venenatum*, *Humicola insolens*, *Humicola lanuginosa*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*, *Penicillium purpurogenum*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei*, or *Trichoderma viride* strain.  
15

14. The method of claim 4, 5, 7, or 8, wherein the polypeptide is obtained from *Aspergillus*, e.g., *Aspergillus aculeatus*, *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger*, or *Aspergillus oryzae*.  
20

15. The method of any of claims 1-14, wherein the one or more additional proteases are endopeptidases.

16. The method of claim 15, wherein the endopeptidase is a glutamyl endopeptidase (EC  
25 3.4.21.19); a lysyl endopeptidase (EC 3.4.21.50); a leucyl endopeptidase (EC 3.4.21.57); a glycyl endopeptidase (EC 3.4.22.25); a prolyl endopeptidase (EC 3.4.21.26); trypsin (EC 3.4.21.4) or a trypsin-like (lysine/arginine specific) endopeptidase; or a peptidyl-Asp metalloendopeptidase (EC 3.4.24.33).

17. The method of any of claims 1-16, wherein the one or more additional proteases are  
30 an exo-peptidase that may act from either end of the peptide.

18. The method of claim 17, wherein the exopeptidase is an aminopeptidase such as a leucyl aminopeptidase (EC 3.4.11.1); a dipeptide aminopeptidase or a tripeptide aminopeptidase (EC 3.4.11.4).

5

19. The method of claim 18, wherein the exopeptidase is a carboxypeptidase such as a proline carboxypeptidase (EC 3.4.16.2); a carboxypeptidase A (EC 3.4.17.1); a carboxypeptidase B (EC 3.4.17.2); a carboxypeptidase C (EC 3.4.16.5); a carboxypeptidase D (EC 3.4.16.6); a lysine (arginine) carboxypeptidase (EC 3.4.17.3); a  
10 glycine carboxypeptidase (EC 3.4.17.4); an alanine carboxypeptidase (EC 3.4.17.6); a glutamate carboxypeptidase (EC 3.4.17.11); a peptidyl-dipeptidase A (EC 3.4.15.1); or a peptidyl-dipeptidase (EC 3.4.15.5).

20. The method of any of claims 1-14, wherein the one or more additional proteases is a  
15 mixture of proteases obtained from *Aspergillus oryzae*-strain 1568.

21. The method of any of claims 1-20, further comprising adding to the proteinaceous material one or more other enzymes selected from the group consisting of amylase, carbohydrase, cellulase, esterase, alpha-galactosidase, beta-galactosidase, glucoamylase,  
20 alpha-glucosidase, beta-glucosidase, lipase, pectinolytic enzyme, peptidoglutaminase, phytase, transglutaminase, or xylanase.

22. The method of any of claims 1-21, wherein the proteinaceous material is a foodstuff of animal origin, preferably milk protein, whey protein, casein, meat protein, fish protein,  
25 blood protein, egg white gelatin, or lactoalbumin.

23. The method of any of claims 1-21, wherein the proteinaceous material is a foodstuff of vegetable origin, preferably soy protein, grain proteins, *e.g.*, wheat gluten, corn gluten, barley, rye, oat, rice, zein, lupine, cotton seed protein, rape seed protein, peanut, alfalfa  
30 protein, pea protein, fabaceous bean protein, sesame seed protein, or sunflower.

24. A protein hydrolysate produced by any of the methods of claim 1-12.
25. A protein hydrolysate of claim 24 which is enriched in free glutamic acid and/or peptide bound glutamic acid residues
- 5
26. A food product or an animal feed additive comprising a protein hydrolysate of claim 24 or 25.

1/12

ATGAGGTCGCTTTTGTGGCTTCGTTGCTTTTCGGGGCGTGTGGCTGGGAGGGCGCTTGTTTCGCCGGATGAGTTCGCCGAGGATATTCAG 90  
M R S L L W A S L L S G V L A G R A L V S P D E F P E D I Q  
 TTGGAAGATCTGCTGGAAGGATCCCAACAGCTTGAGGACTTCGCCTATGCCTACCCCGAGCGCAATCGCGTCTTTGGTGGTAAAGCCAC 180  
L E D L L E G S Q Q L E D F A Y A Y P E R N R V F G G K A H  
 GACGACACGGTTAACTATCTCTACGAGGAGCTGAAGAAGACTGGCTACTATGATGCTACAGCAGCCTCAGGTGCAGGTGTGGAGCAAT 270  
 D D T V N Y L Y E E L K K T G Y Y D V Y K Q P Q V H L W S N  
 GCCGACCAGACGCTCAAGGTGGCGGATGAGGAAATCGAGGGGAAGACCATGACCTACAGTCCAGCGTCGAGGTCACGCCGCGATGTAGCC 360  
A D D T L K V G D E E I E A K T M T Y S P S V E V T A D V A  
 GTCGTCAAGAACCTGGGATGCAGCGAGGCGGATTACCCATCCGATGTCGAGGGCAAGCTCGCCCTGATCAAGCGTGGAGAATGCCCGTTC 450  
V V K N L G C S E A D Y P S D V E G K V A L I K R G E C P F  
 GCGGACAAGTCGGTTCTCGCTGCCAAAGCCAAAGCGCGGCTTCGATTGTCTATAACAATGTGGCCGGATCCATGGCGGGCACCCCTTGGC 540  
 G D K S V L A A K A K A A A S I V Y N N V A G S M A G T L G  
 GCGGCGCAGAGTGATAAGGACCGTATTTCGGCCATTGTCGGTATCAGCTTGGAGGATGCCAGAAGCTGATCAAGCTTGCTGAGGCTGGA 630  
 A A Q S D K G P Y S A I V G I S L E D G Q K L I K L A E A G  
 TCGGTATCTGTGGATCTGTGGTGGATAGTAAGCAGGAGAACCCTACGACGTATAACGTTGTGCGCAGACGAAGGGCGGCGATCCGAAC 720  
 S V S V D L W V D S K Q E N R T T Y N V V A Q T K G G D P N  
 AACGTCGTCGCGCTGGGTGGCCACACGGACTCAGTCGAGGGCGGCCCTGGTATCAACGACGATGGCTCGGGCATTTATTAGCAACTTGGTC 810  
 N V V A L G G H T D S V E A G P G I N D D G S G I I S N L V

FIG.1A

ATTGCCAAGCGCTCAGCAGTACTCGGTCAAGAAATGCCGTGGCTTCCCTCTTCTGGACAGCAGAGGATTTCGGTCTGCTGGGCAGCAAC 900  
I A K A L T Q Y S V K N A V R F L F W T A E E F G L L G S N  
TACTACGTCTCCCATCTGAATGCCACCGAGCTGAACAAGATCCGACTGTACCTGAACCTTCGACATGATCGCCTCACCTAACTACGCCCTC 990  
Y Y V S H L N A T E L N K I R L Y L N F D M I A S P N Y A L  
ATGATCTATGACGGTGATGGATCGGGTTCAACCAAGAGCGGACCGCGGTTCCGCCCCAGATCGAGAAACTGTTCGAGGACTACTACGAC 1080  
M I Y D G D G S A F N Q S G P A G S A Q I E K L F E D Y Y D  
TCCATCGACCTGCCTCATATCCCCACCCAGTTTGACGGACGTTCCGACTACGAGGCCCTTTATCCTGAACGGCATTCCGTCCGGTGGACTC 1170  
S I D L P H I P T Q F D G R S D Y E A F I L N G I P S G G L  
TTCACGGGCGCGAGGGCATCATGTCCGAAGAGAACGCAAGCCGCTGGGGAGGTCAGCCGGCTGGCCTACGACGCCCAACTACCACGCC 1260  
F T G A E G I M S E E N A S R W G G Q A G V A Y D A N Y H A  
GCGGGAGACAACATGACCAACCTCAACCATGAAGCCTTCCTGATCAACTCCAAGCCACCGCCTTCGCCGTGCGCACCTACGCCCAACGAC 1350  
A G D N M T N L N H E A F L I N S K A T A F A V A T Y A N D  
CTCTCCTCGATCCCCAAGGGAATACCACATCCTCTTGCACCGAGCCCGCACCATTCGACCATTCGGCAAGAGAGCTCCGAAGACA 1440  
L S S I P K R N T T S S L H R R A R T M R P F G K R A P K T  
CAGGCTCAGGTATCAGGATCCGGATGCTGGCATTCCTCAAGTCGAGGCATAG 1491  
H A H V S G S G C W H S Q V E A

FIG.1B

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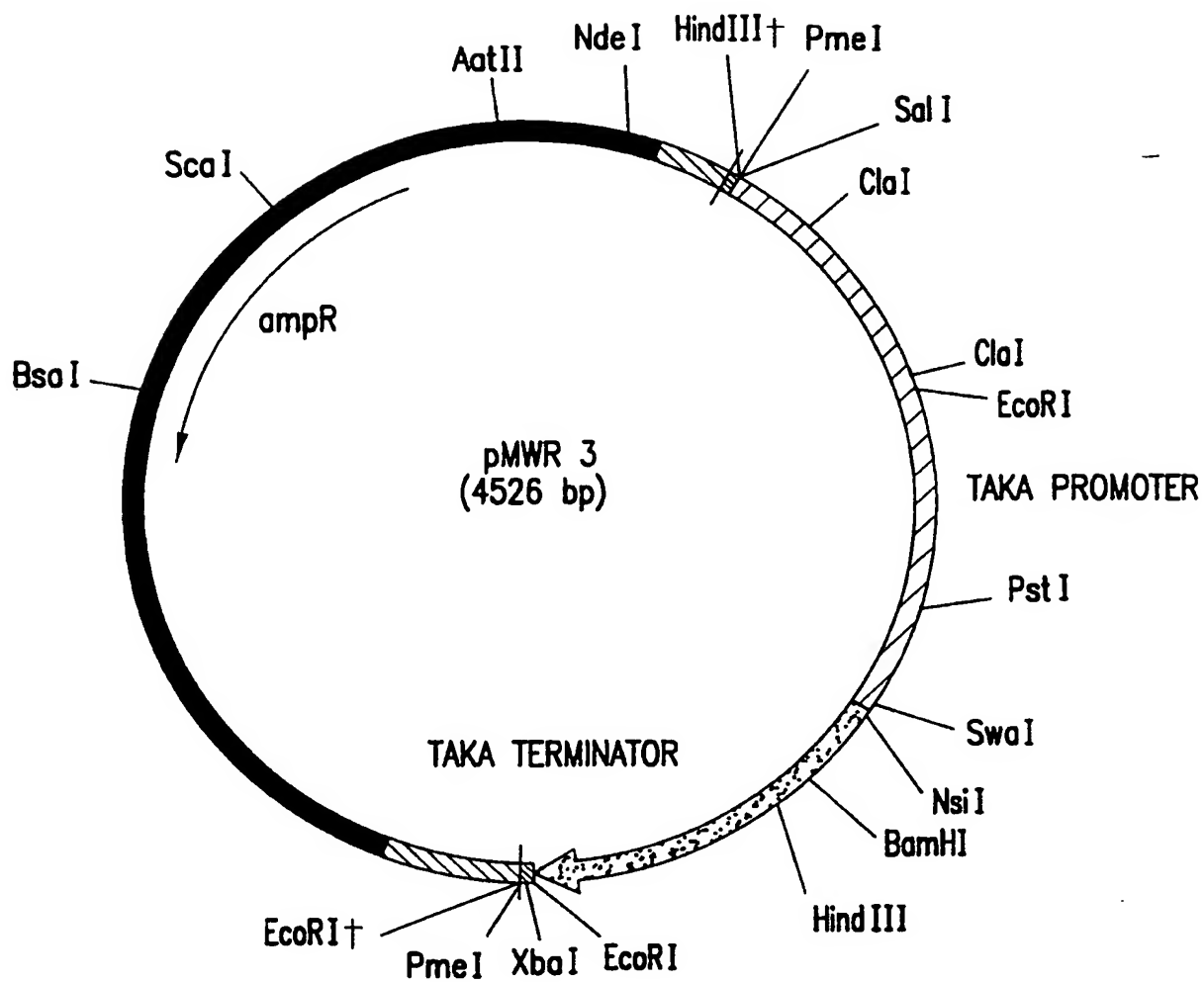


FIG.2

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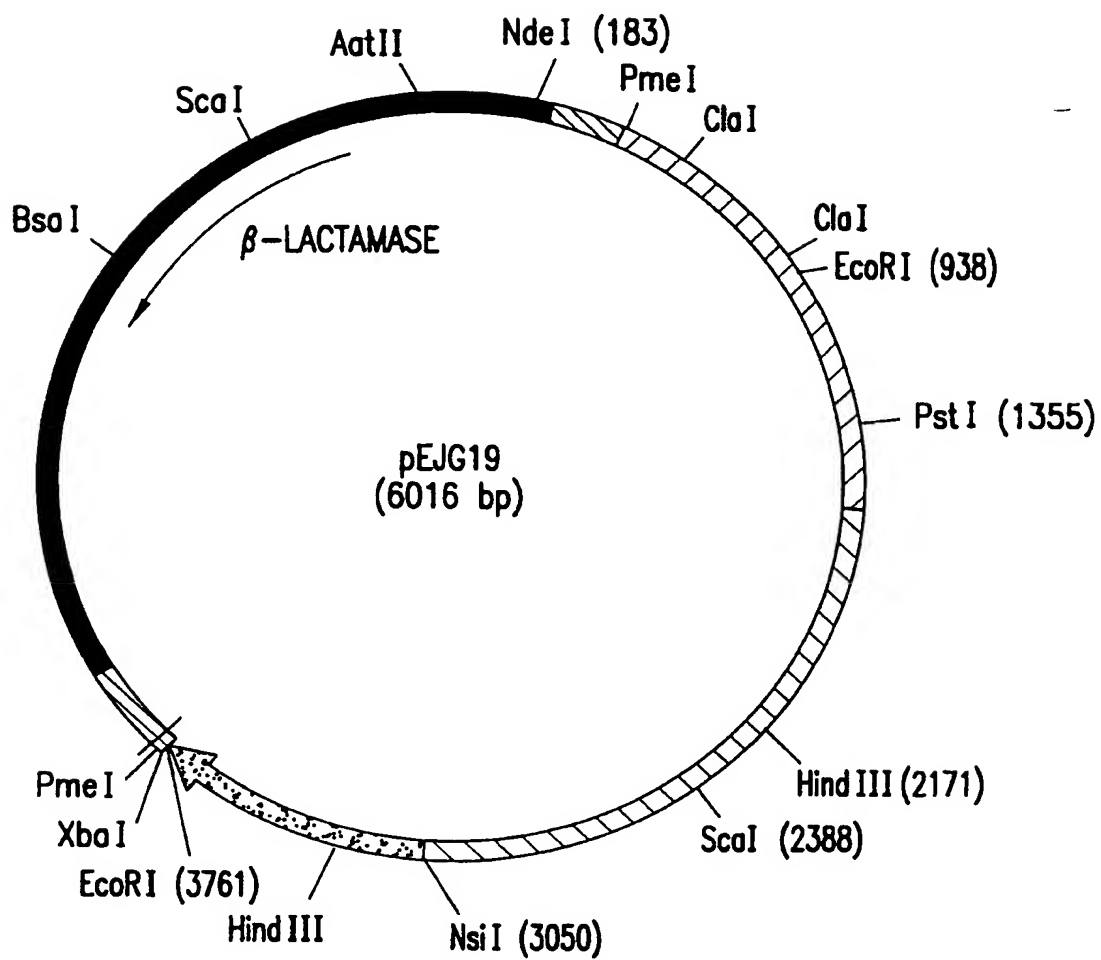


FIG.3

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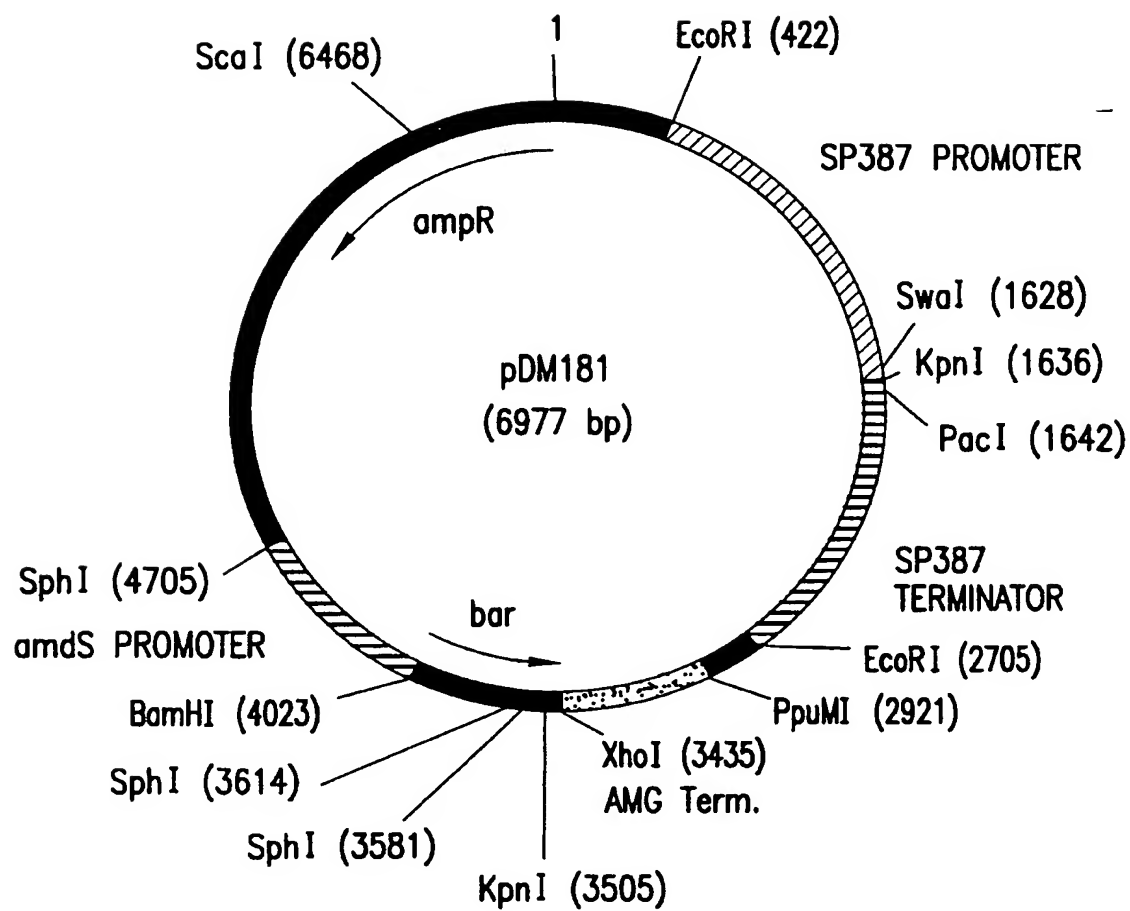


FIG.4

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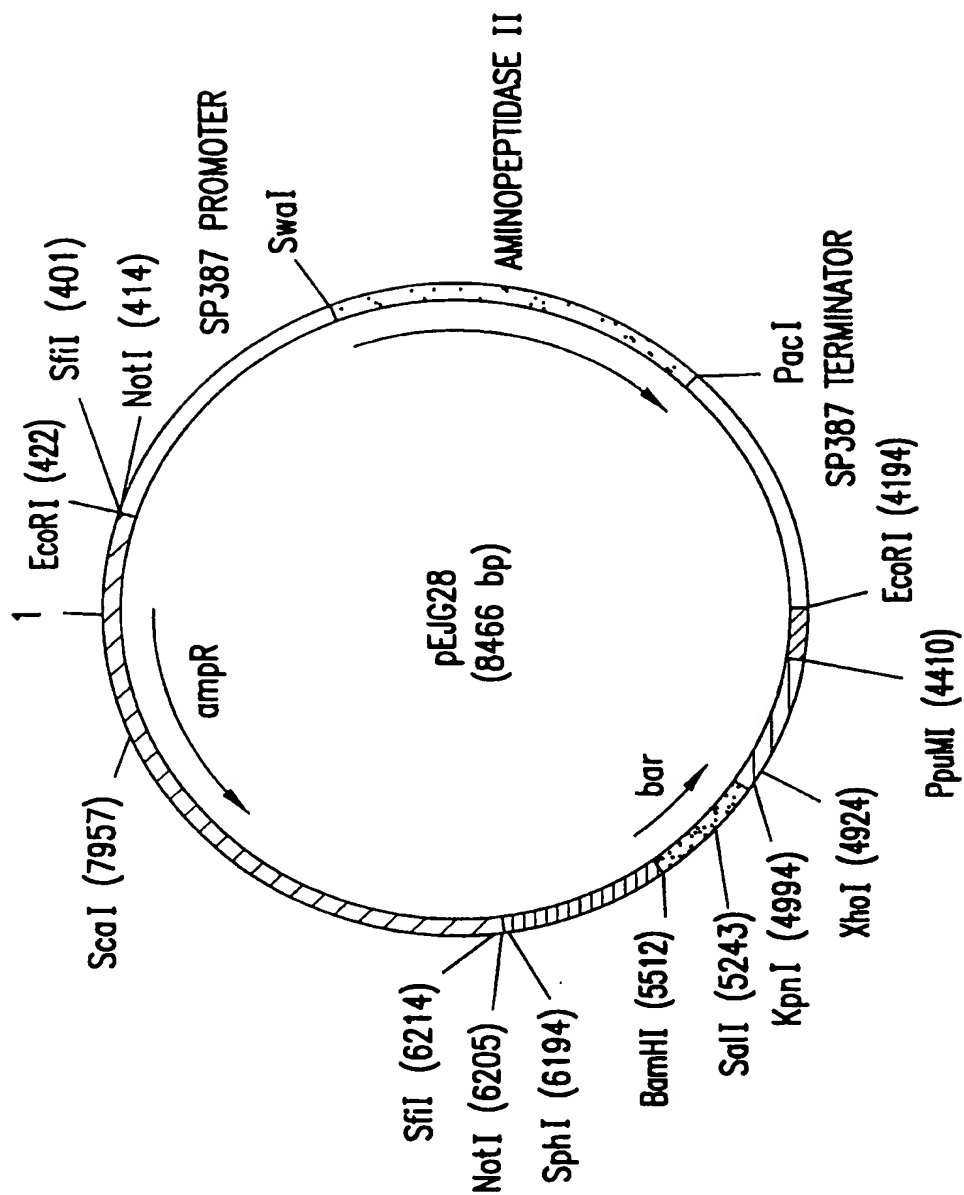


FIG.5

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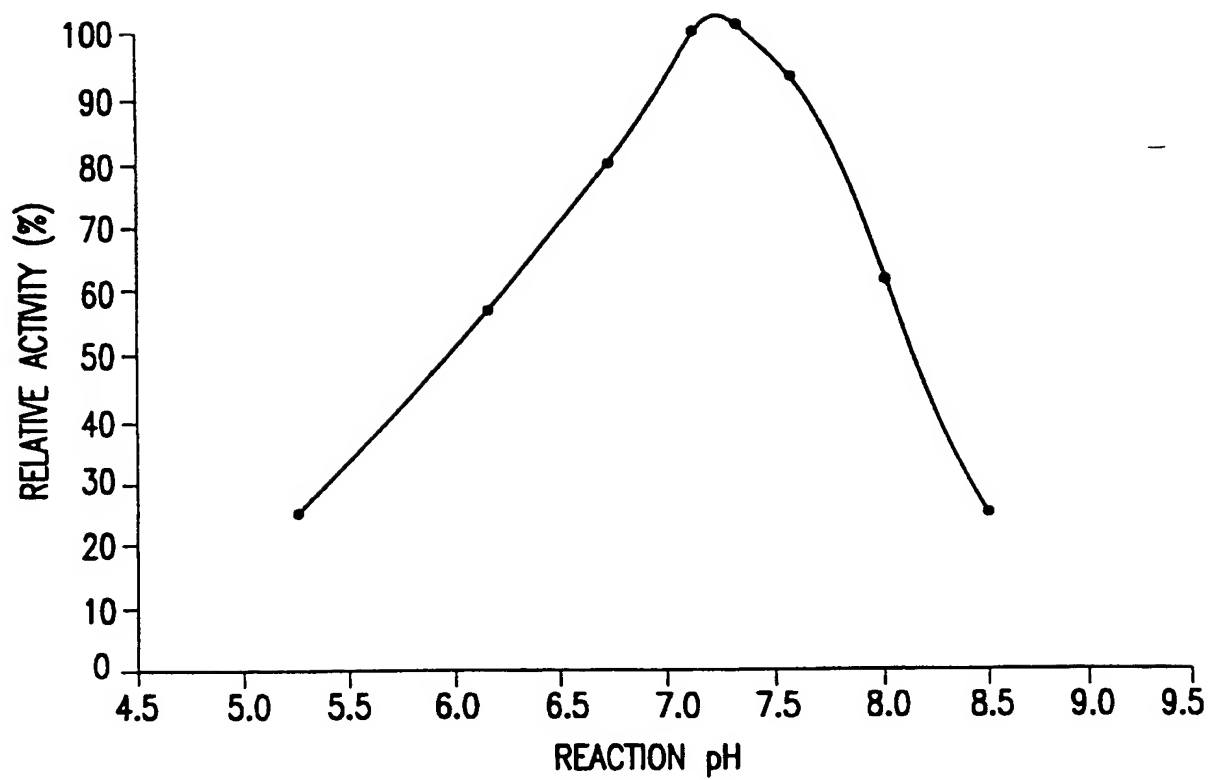


FIG.6

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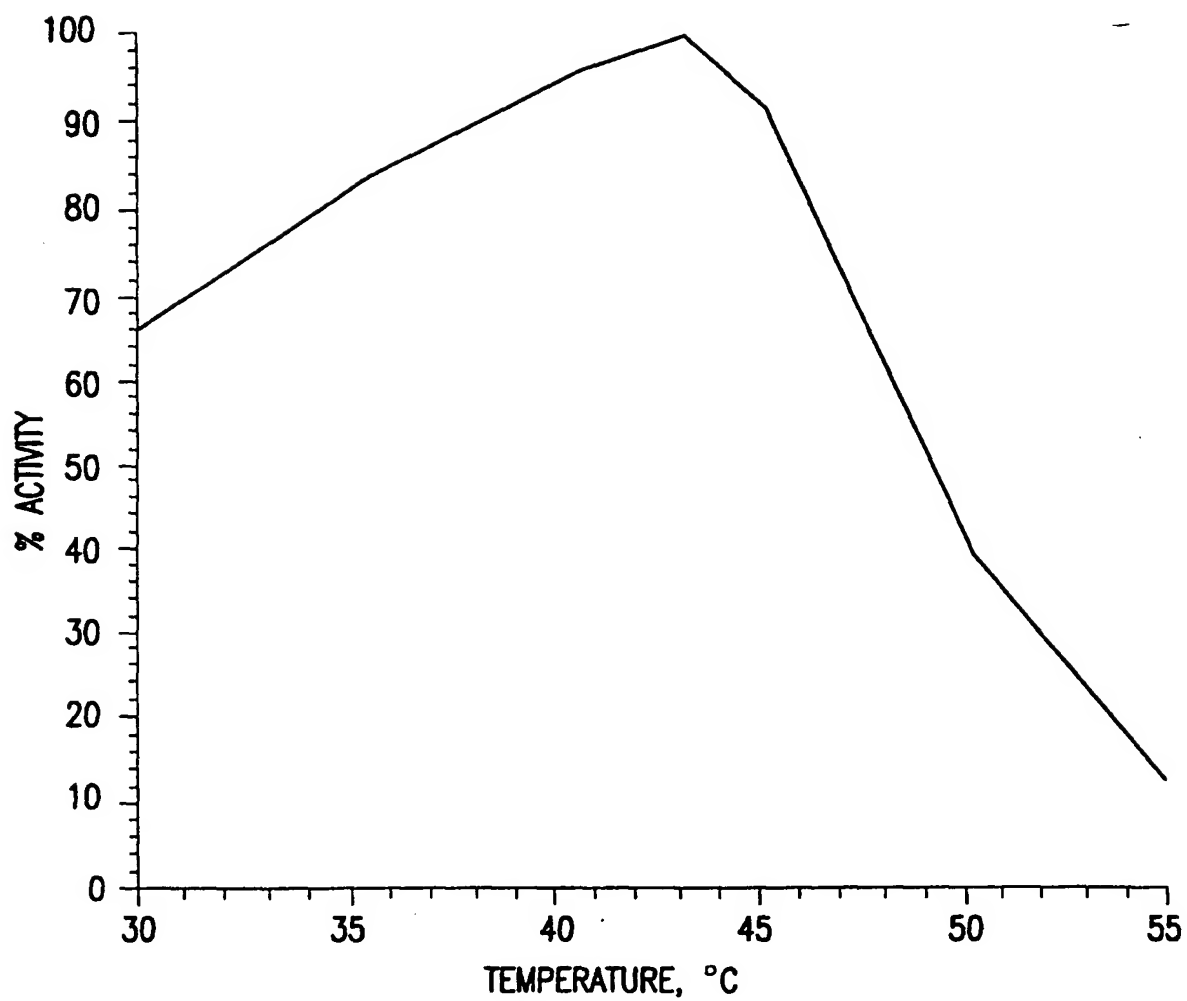


FIG.7

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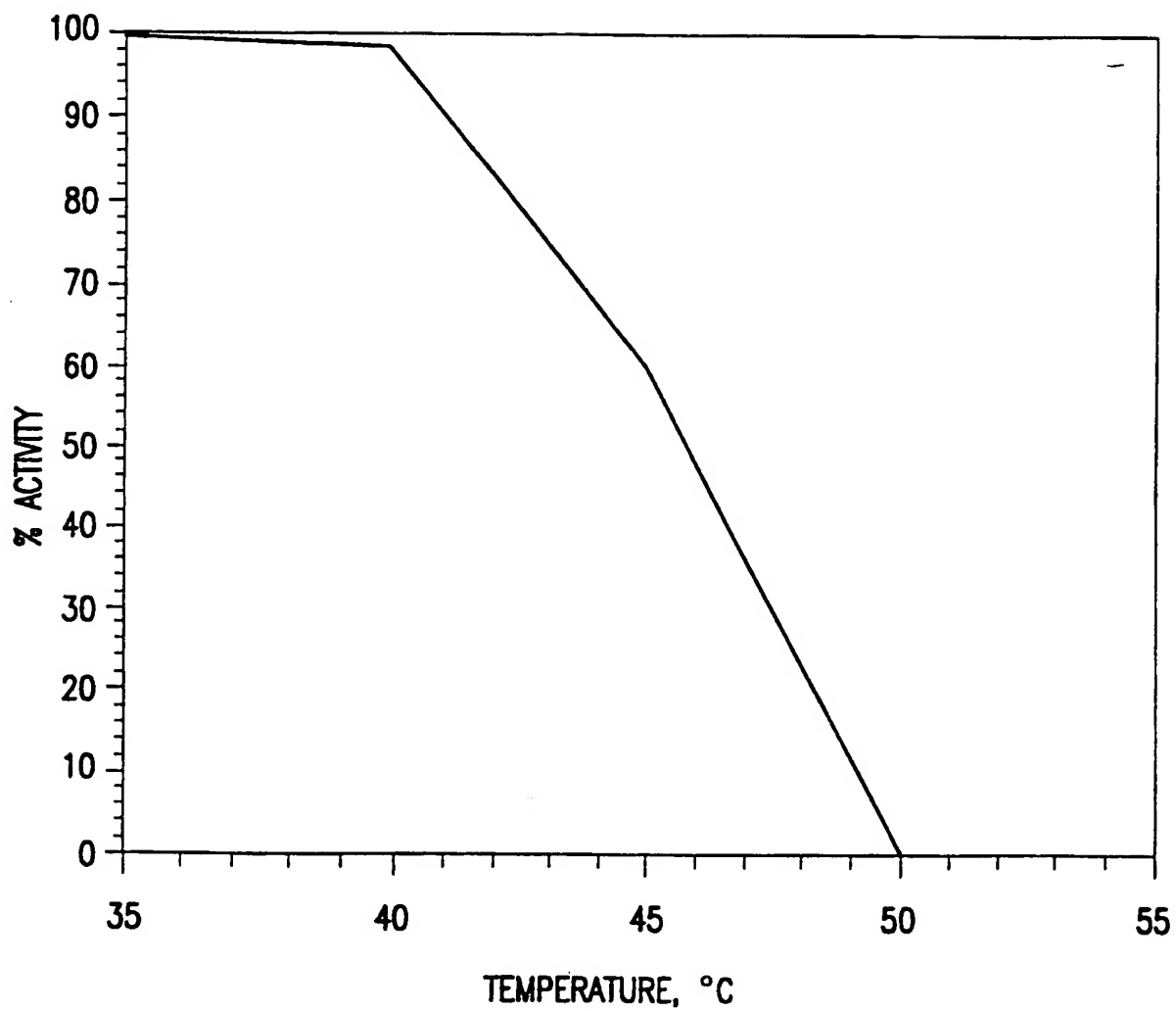


FIG.8

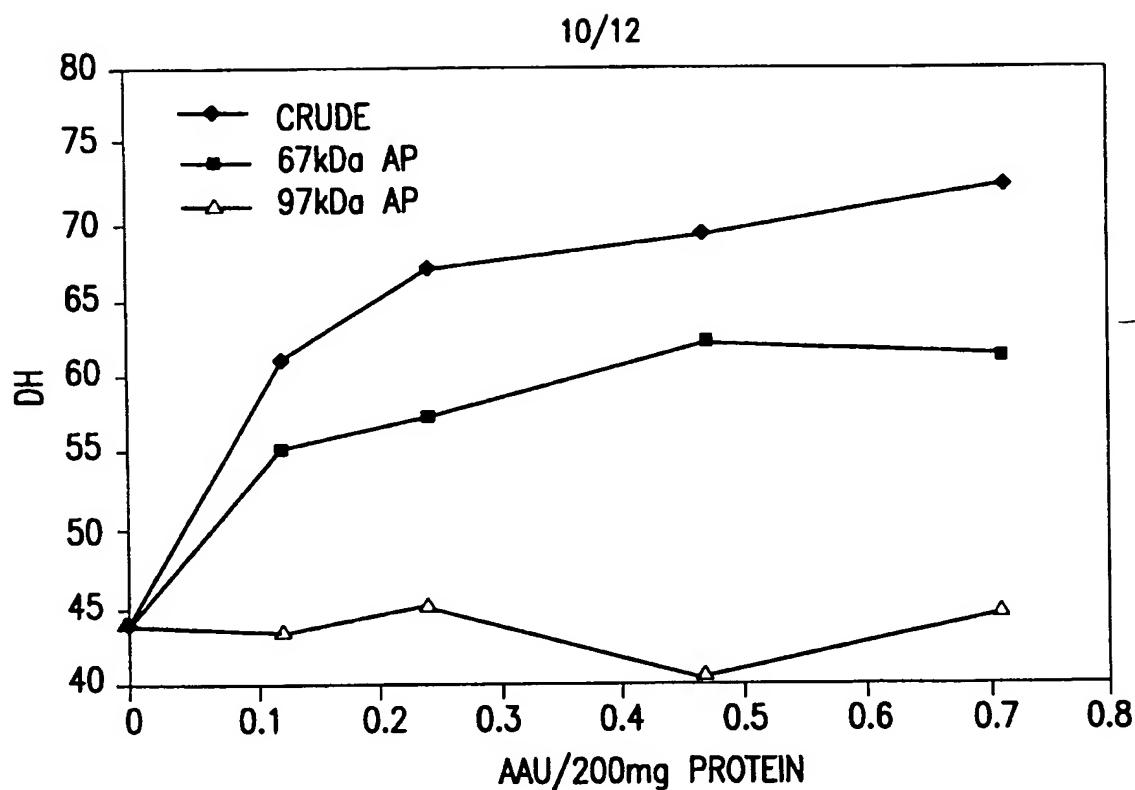


FIG.9

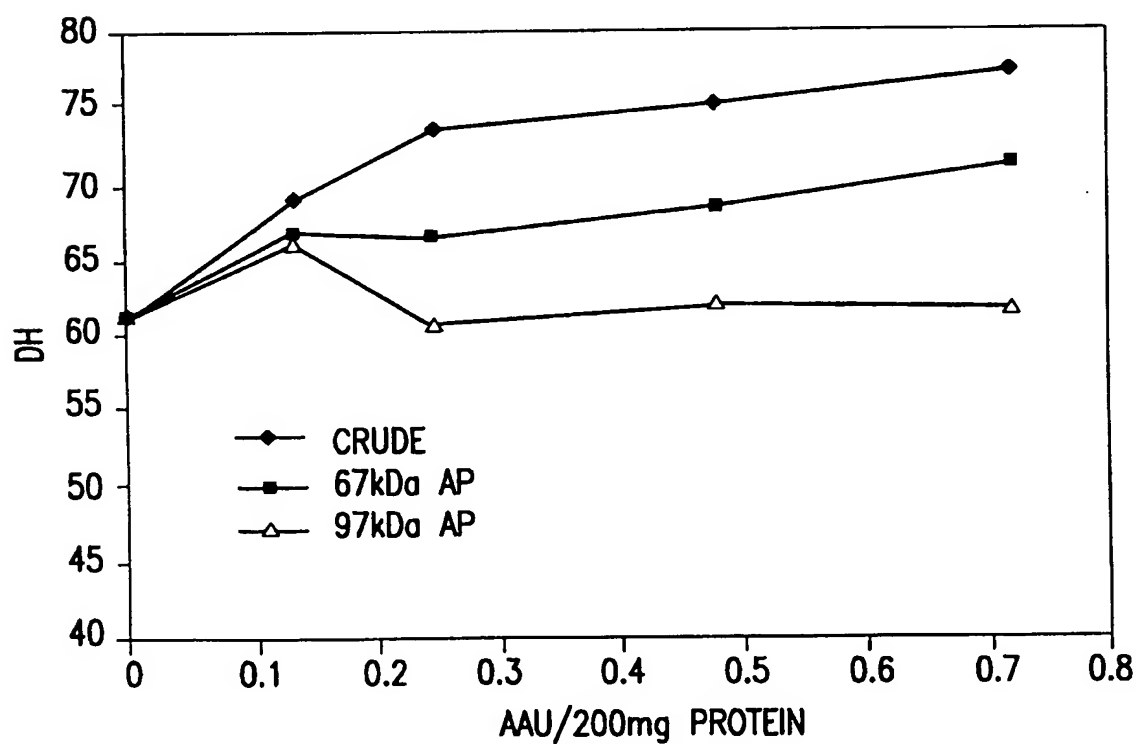


FIG.10

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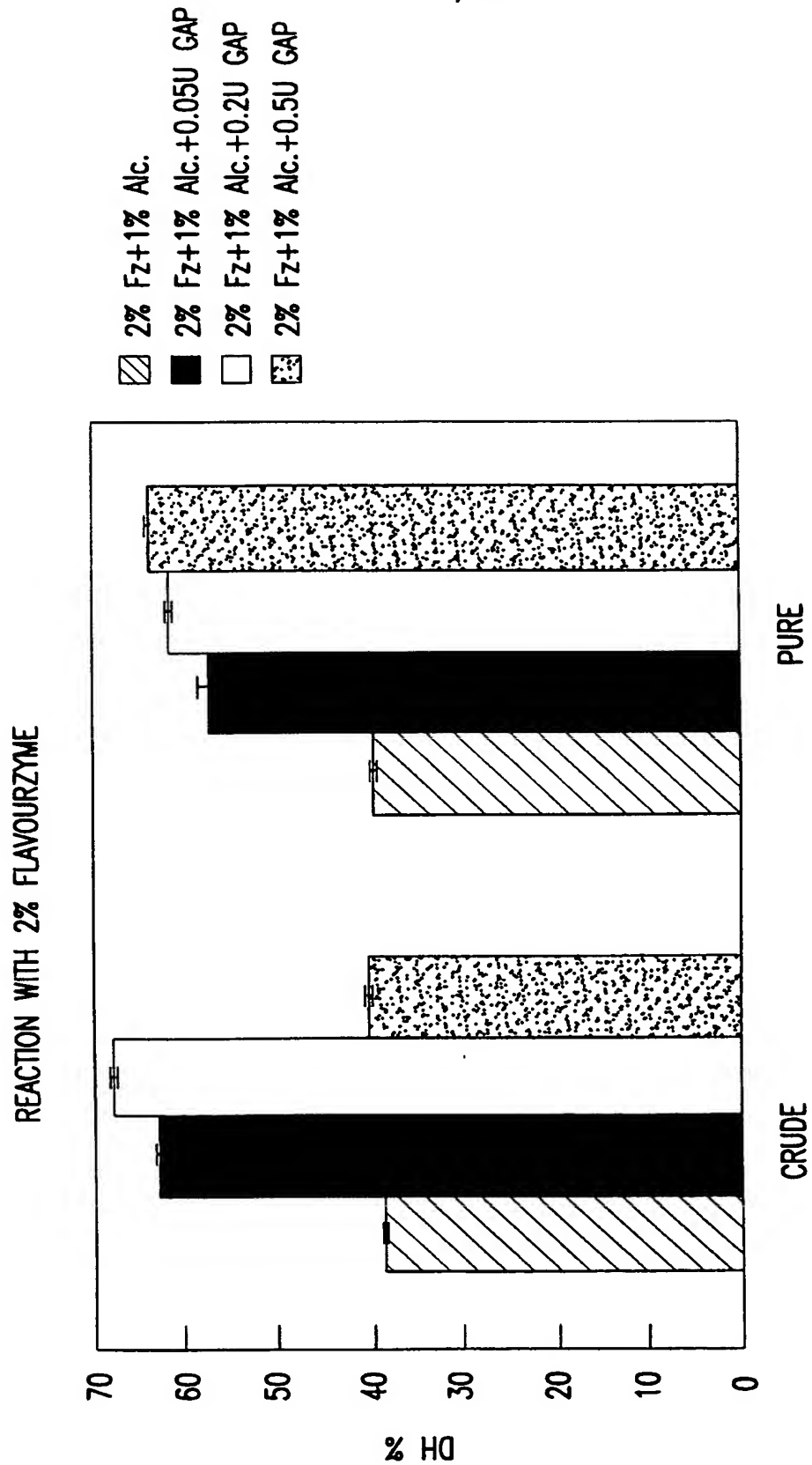


FIG. 11

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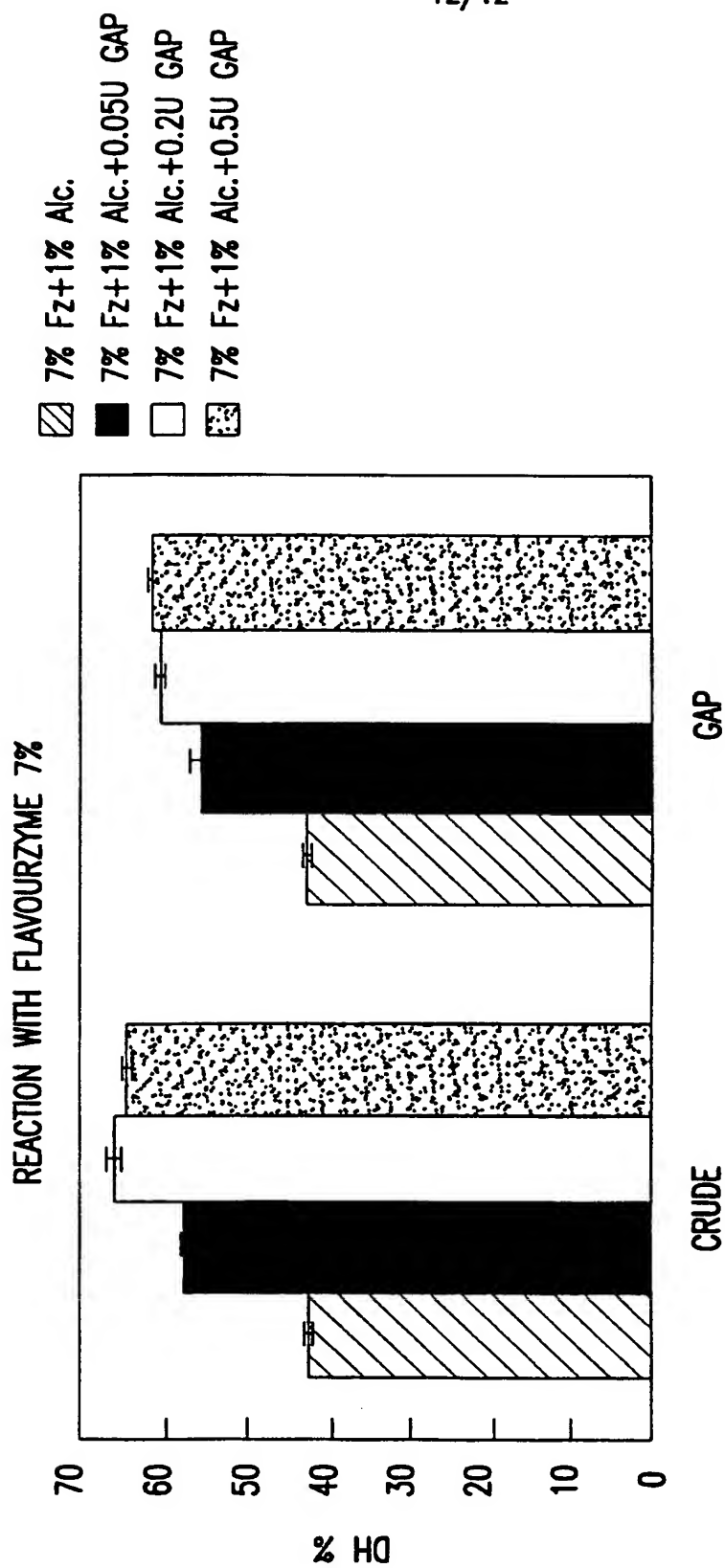


FIG.12

Applicant's or agent's file reference number	5253.504-WO	International application To Be Assigned	PCT/US 98/09998
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13 bis)

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A. The indications made below relate to the microorganism referred to in the description on page <u>55</u> , lines <u>10-16</u>	
B. IDENTIFICATION OF <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depository institution Agricultural Research Service Patent Culture Collection (NRRL)	
Address of depository institution (including postal code and country)  Northern Regional Research Center 1815 University Street Peoria, IL 61604, US	
Date of deposit April 4, 1997	Accession Number NRRL B-21677
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
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